

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model  
Run on: May 25, 2003, 08:48:53 ; Search time 2746 Seconds  
(without alignments)  
10958.595 Million cell updates/sec

Title: US-09-955-526-3  
Perfect score: 1034  
Sequence: 1 gagcaacataacattgtct.....ataaggaagttctctgtga 1034

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551403878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pa.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_ss.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_hg\_hum.\*  
31: em\_hg\_inv.\*  
32: em\_hg\_other.\*  
33: em\_hg\_mus.\*  
34: em\_hg\_pln.\*  
35: em\_hg\_rod.\*  
36: em\_hg\_man.\*  
37: em\_hg\_vrt.\*  
38: em\_sy.\*  
39: em\_hgco\_hum.\*  
40: em\_hgco\_mus.\*  
41: em\_hgco\_other.\*

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	52.7	545	1293	8	AF390556	AF390556 Nicotiana
2	41.5	428.8	1066	8	AY087532	AY087532 Arabidops
3	41.3	427.2	994	8	AY091134	AY091134 Arabidops
4	41.3	427.2	1005	8	AF208124	AF208124 Arabidops
5	41.3	427.2	1117	8	AB025927	AB025927 Arabidops
6	40.6	420.2	775	8	AY114059	AY114059 Arabidops
7	40.4	418	1010	8	AF390555	AF390555 Brassica
8	40.0	413.4	1013	8	AF453320	AF453320 Brassica
9	38.6	399.2	1019	8	AF453321	AF453321 Brassica
10	33.9	351	1181	8	AB025926	AB025926 Oryza sat
11	33.4	345.4	744	8	HVU290421	AJ290421 Hordeum v
12	17.3	178.6	418	11	G73645	G73645 RZ957F etio
13	13.3	137.2	360	11	G71526	G71526 AG1521534FM
14	12.1	125.2	892	9	AF033095	AF033095 Homo sapi
15	12.1	125.2	2609	9	BC000916	BC000916 Homo sapi
16	11.9	122.8	1745	5	AF220548	AF220548 Paralicit
17	11.8	122	2600	9	HSTEGT	X75861 H.sapiens T
18	11.8	122	2634	6	AR058920	AR058920 Sequence
19	11.8	122	2634	6	AR058921	AR058921 Sequence
20	11.8	122	2634	6	AR112791	AR112791 Sequence
21	11.8	122	2634	6	AR112792	AR112792 Sequence
22	11.6	119.8	2331	10	BC005588	BC005588 Mus muscu
23	11.0	113.8	3498	8	AB025609	AB025609 Arabidops
24	10.5	108.4	896	10	RNTEGT3	X75856 R.horvegicu
25	10.5	108.4	940	10	RNTEGT2	X75855 R.horvegicu
26	9.1	94.6	127507	2	AF005311	AF005311 Oryza sat
27	9.1	94.6	155492	2	AF005304	AF005304 Oryza sat
28	8.5	87.4	198788	8	ATCNRIV46	ATCNRIV46 Arabidops
29	8.5	87.4	207674	8	ATFCA8	297343 Arabidops
30	5.5	57	202	6	EL5289	EL5289 Oryza sativ
31	5.3	54.8	47460	8	AB011478	AB011478 Arabidops
32	4.7	48.8	7218	6	I66494	I66494 Sequence 14
33	4.7	48.2	1141	6	AX083744	AX083744 Sequence
34	4.6	47.8	6741	6	B32987	E32987 Gene encodi
35	4.4	46	5100	9	AF084196	AF084196 Pan trogl
36	4.4	46	7436	9	AF061786	AF061786 Homo sapi
37	4.4	46	72871	2	AC091550	AC091550 Homo sapi
38	4.4	46	108122	2	AC116905	AC116905 Homo sapi
39	4.4	46	153077	9	AC020679	AC020679 Homo sapi
40	4.4	46	170558	2	AC012414	AC012414 Homo sapi
41	4.4	46	184108	2	AC023191	AC023191 Homo sapi
42	4.4	46	211391	2	AC037471	AC037471 Homo sapi
43	4.4	45.2	6849	2	AC118646	AC118646 Mus muscu
44	4.4	45.2	6849	2	AC118646	AC118646 Mus muscu
45	4.4	45.2	68931	2	AC117831	AC117831 Mus muscu

ALIGNMENTS

RESULT 1  
AF390556  
LOCUS AF390556 1293 bp mRNA linear PLN 16-JUL-2001  
DEFINITION Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds.  
ACCESSION AF390556  
VERSION AF390556.1 GI:14719275  
KEYWORDS  
SOURCE Nicotiana tabacum.  
ORGANISM Nicotiana tabacum.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 1293)  
AUTHORS Bolduc,N., Pitre,F. and Brisson,L.  
TITLE Characterization of Bax inhibitor 1 from Nicotiana tabacum

Pred. No. is the number of results predicted by chance to have a

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1293)  
AUTHORS Bolduc, N., Pitre, F. and Brisson, L.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval  
University, Quebec G1K 7P4, Canada  
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Location/Qualifiers  
source 1..1293  
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CDS 134..883  
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BASE COUNT 296 a 243 c 304 g 450 t  
ORIGIN

Query Match 52.78; Score 545; DB 8; Length 1293;  
Best Local Similarity 83.28; Pred. No. 1.5e-134;  
Matches 633; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 75 AAGAAGAGAACATGGAAGTTTCACATCGTTCCTCGACTCGCAATCTG---CCTCTCGC 131  
DB 122 AAGAAGAGAGAAATGGAGCTTGGACATCGTTCCTCAATTCACATCGCGGTCTCTCGC 181  
QY 132 AACCGCTGAGTATGATTCTCTCAAAACATCCGCCAGATCTCACCTCTCGTTCAAAC 191  
DB 182 ATCTCTGAGTTAGATCTCTTAAAGACTTCGCCAGATCTCTCCCTTGTTCAACT 241  
QY 192 CATCTCAAGAGGTGACTTACCGTATCTGTGCTTTAGTGGCATCGGTCTGTGGGCT 251  
DB 242 CATCTCAAAAGGTCTACCTTTCAATATGTTGTGCTTTAGTGTCTCGGTCTGTGGGCT 301  
QY 252 TACCTTCACATCTATGAATATCGTGGCTCTCTCACAAATGGCTTCATCGGGAAGC 311  
DB 302 TACCTTCACATCTTTGGAACATATGTTGCTTACTTACGACATGGAGATGTTGGAGC 361  
QY 312 ATGGTGTGCTTCTCTAGCTCTCTTATCAAGAGCAAAAGGGTGGCTCTTCTGATG 371  
DB 362 ATAGTGTGCTGATGGCAGACCTCTGTATGAGAGCAAAAGAGATAGCACATCTGATG 421  
QY 372 GCAGCTGCATTTTGAAGGCGCTCTATTGCTCTGTATGAGCTGGGCATTAACCTC 431  
DB 422 GCAGCTGCATCTTTAAGAGGACATCTATTGGTCCACTGATTAATTTGGCTATGACTTT 481  
QY 432 GATCCAAGCATTTGTTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGTTGCTTCTCA 491  
DB 482 GACCCAAGCATTTGATCGGTCTTTTGTGTTGTGCTGTGCTTTGTTGCTTCTCA 541  
QY 492 GCTGTGCTCATCTTGGCAGGCGAGGAGTACTTACTTCGGGCGCTTCTTCTATCT 551  
DB 542 GCTGTGCTCATCTTGGCAGGCGAGGAGTACTTATCTTTGGAGCTCTCTTCTATCT 601  
QY 552 GGCGTCTCCCTCTCTTCTGTGTGACCTTTGATCCCTCCCAATTTTGGTGTTCATGGCT 611  
DB 602 GGTCTCTCATCTTTTCTGTTGTGACCTTCGCTCGCTCCCTCCATTTTGGTGTTCATGGC 661  
QY 612 GTTTCAGTTTGTGTTATTTTGGACTCTTGTGTTTGTGGCTACATCGTCTTGAC 671  
DB 662 TTGTTCAAGTTCTGAGTTTATTTTGGGCTCTTGTGTTTGTGGGCTATATCATTTTGAC 721  
QY 672 ACCCAAGAAATTAATGAGAAGGCTCACTTGGGTGATGATGATTACGTTAAGCATGCACTG 731

DB 722 ACCAAGATATAATTGAGAAGGCACACCTTGGGATTTGGACTACGTGAAGCATCTCTG 781  
QY 732 ACCCTTTTCACAGATTTCGCGCTGTTTTCGCGGANTTCGATCATCATGTTAAGAAT 791  
DB 782 ACCCTCTTTACAGATTTCGCTGTTTTCGCGAATATTATCATATGCTGAAGAT 841  
QY 792 GCATCTGAGAGGAAGAGAGAGAGAGAGAGAGAGAGAACTA 832  
DB 842 GCATCCGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAACTA 882

RESULT 2  
AY087532 1066 bp mRNA linear PLN 26-JUN-2002  
LOCUS Arabidopsis thaliana clone 36400 mRNA, complete sequence.  
DEFINITION Arabidopsis thaliana  
ACCESSION AY087532  
VERSION AY087532.1 GI:21406269  
KEYWORDS FLI CDNA.  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 1066)  
AUTHORS Haas, B.J., Volfovsky, N., Town, C.D., Trukhan, M., Alexandrov, N.,  
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.  
TITLE Full-length messenger RNA sequences greatly improve genome  
annotation  
JOURNAL Genome Biol. (2002) In press  
REFERENCE 2 (bases 1 to 1066)  
AUTHORS Brover, V., Trukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feldmann, K.  
TITLE Full-length cDNA from Arabidopsis thaliana  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1066)  
AUTHORS Brover, V., Trukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feldmann, K.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made  
available to TIGR and GenBank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have  
frame shifts in a coding region. A sequence is considered to be  
5'-truncated if it lacks the translation initiation start (ATG). A  
sequence is considered to be 3'-truncated if it lacks the  
C-terminal end of the encoded protein. Please note that these cDNA  
sequences are derived from the Ws or Laer ecotypes and therefore  
may contain polymorphisms when compared to sequences from Col-0.  
GenSet carried out the library production and sequencing of the  
full-length clones. Ceres, Inc. carried out the clustering of the  
5' sequences, selection of clones, and sequence assembly.

FEATURES  
source 1..1066  
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DFVAVFVIRILLMLNKSADKEKKRRN"  
BASE COUNT 268 a 205 c 224 g 369 t

ORIGIN	1;	AUTHORS	Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.						
Query Match	41.5%;	Score	428.8;	DB 8;	Length	1066;			
Best Local Similarity	73.7%;	Pred. No.	1.6e-103;						
Matches	560;	Conservative	0;	Mismatches	197;	Indels	3;	Gaps	
2Y	72	AGAGAAGAGAACATGGAAGTTTCACATGTTCTTCGACTCGCATCTCGCTCTCGC	131						
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2Y	132	AACCGCTGGAGTTATGATTTCTCAAAACATTCGCCAGATCTCACCTCTCGTTCAAACT	191						
Db	91	AGAGCTGGAGCTATGATTTCTTAAACATTCCTCGATTTCTCCAGCGTTCCAGAT	150						
QY	192	CATCTCAACAGAGTACCTTACGTTATGCTGTCTTATGTCGATCGCTCGCTGGGCT	251						
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QY	312	ATGGTGTGGCTTCTTCAGCTCCTCTTATCAGAGCAAAAAGGGTCTTCTCTGATG	371						
Db	271	ATGATTTGGCTCTTTCATGCTCTCTTATGAACACCAAAAAGGCTTCTCTCTGTT	330						
QY	372	GCAGCTGCACCTTTTGAAGCGCCCTTATTTGGTCTCTGATTTGAGCTGGCATTAACCTC	431						
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QY	552	GGGCTCTCCCTTCTCTTCTGCTTGTGCACTTGTGATCTCCATTTTGTGTTGCTTCCATG	611						
Db	511	GGCTGTCTATGCTATGCTTGTGCTCCAGTTTGTCTTCTGATCTTGTGCTCTCATCT	570						
QY	612	GTCTTCAAGTTGAGTTGATTTTGGACTCTTGTGTTGTGGGCTCATGCTCTTTCAC	671						
Db	571	ATCTTTAAGTTTGAAGTTGATTTTGGACTTTTGAATCTTGTGGGATCATGTTGGTGGAC	630						
QY	672	ACCAAGAAATTTATGAGAGGCTCACTTGGGTGATGATGATTACGTTAAGCATCATTTG	731						
Db	631	ACACAGAGATTTATGAAAGGACACCTCGTGACATGACATGTAATAACATTCGTTG	690						
QY	732	ACCTTTTCAAGATTTTGGCGCTGTTTGTGCGGATTTCTGATCATCATGTTAAAGAT	791						
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RESULT 3	AY091134	Arabidopsis thaliana putative Bax inhibitor-1	994 bp	mRNA	linear	PLN 22-APR-2002			
LOCUS	AY091134	Arabidopsis thaliana putative Bax inhibitor-1 (At5g47120)	mRNA						
DEFINITION	complete cds.								
ACCESSION	AY091134	GI:20268759							
KEYWORDS	FLI CDNA.								
SOURCE	Arabidopsis thaliana.								
ORGANISM	Arabidopsis thaliana.								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;								
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TITLE	2	(bases 1 to 994)							
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REFERENCE	2	(bases 1 to 994)							
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TITLE	2	(bases 1 to 994)							
JOURNAL	2	(bases 1 to 994)							
REFERENCE	2	(bases 1 to 994)		</					

Query Match	41.3%	Score 427.2	DB 8	Length 994
Best Local Similarity	73.6%	Pred. No. 4.4e-103	Indels	3
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Db	22	AAAAAACAAGAACAAATGATCGTTCTTCCTTCCTTCGATTCTCAACCTG---GTAGC	78	
QY	132	AACCGGTGGAGTTATGATTTCTCTMAAAACTTCGCCAGATCTCACTCTCGTTCAACT	191	
Db	79	AGAAGCTGGAGTATGATTTCTCTTAAAACTTCGCTCAGATTTCTCAGCGGTTCAAT	138	
QY	192	CATCTCAACGAGTGCACCTAGCGTATCGTCTCTTTAGTGGCATCGGCTCGGGGCT	251	
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QY	252	TACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGCTTGCAATGGAAGC	311	
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QY	312	ATGGTGTGGCTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGTGGCTCTCTGATG	371	
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Db	319	GTCTCTGCTGTTCTTGAAGGCTCTCTGTTGGCCCTTGATCAAGTGGCAATGATGTT	378	
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QY	492	GCTGCTGCCATGTTGGCAAGCGCAGGAGTACTGTACCTCGGGGCTCTCTTCATCT	551	
Db	439	GCAGCAGCAATGTTAGCAAGCAGGAGTATCTCTACCTTGAGGACTGCTTTCACT	498	
QY	552	GGCGTCTCCCTCTCTCTGTTTGCATTTGCATCTCCATTTTGTGTTGCTCCATGGCT	611	
Db	499	GGTTGTCTATGCTAATGTTGGCTCAGTTTGGCTCTCAATCTTTGTGGCTCTGATCT	558	
QY	612	GTTTTCAAGTTTGAGTTGTTATTTGGACTCTTGCTGTTTGGGCTACATCGCTTTGAC	671	
Db	559	ATCTTTAAGTTTCAGTTGTACTTTTGACCTTTTGTATCTTTTGGGATACATGTTGGTGGAC	618	
QY	672	ACCCAGAAATTAATCAGAAGGCTACCTGGGTGATATGGATTACGTTAAGCATGATG	731	
Db	619	ACACAAGATTAATAGAAAAGGCACCTCGGTGACATGGACTATGTAACAATCTCGTTG	678	
QY	732	ACCTTTTTCACAGATTTTGGCGCTGTTTGTGCGGATCTGATCATCATGTTAAAGAA	791	
Db	679	ACCTTTTTCATGACTTTGTAGCTGTGTTGTTCGATCTTCATCAATAATGTTGAGAAC	738	
QY	792	GCATCTCAGAGGAAGAGAGAAAGAGAGAGAGAACT	831	
Db	739	TCACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAACT	778	

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AF208124	LOCUS	1006 bp	mRNA	linear	PLN 01-DEC-2000
AF208124	DEFINITION	Arabidopsis thaliana Bax inhibitor 1 mRNA, complete cds.			
AF208124	ACCESSION	AF208124			
AF208124.1	VERSION	GI:11493974			
	KEYWORDS				
	SOURCE	Arabidopsis thaliana.			
	ORGANISM	Arabidopsis thaliana			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
		1 (bases 1 to 1006)			
	REFERENCE	Sanchez,P., de Torres Zabaia,M. and Grant,M.			
	AUTHORS	AtB1-1, a plant homolog of Bax inhibitor 1, suppresses Bax-induced			
	TITLE	cell death in yeast and is rapidly upregulated during wounding and			

```

pathogen challenge
Unpublished
2 (bases 1 to 1006)
Sanchez,P., de Torres Zabala,M. and Grant,M.
Direct Submission
Submitted (24-Nov-1999) Biological Sciences, Wye College, Wye,
Ashford, Kent TN25 5AH, UK
Location/Qualifiers
1. 1006
/organism="Arabidopsis thaliana"
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46. .789
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BASE COUNT 246 a 197 c 214 g 349 t
ORIGIN

Query Match 41.3%; Score 427.2; DB 8; Length 1006;
Best Local Similarity 73.6%; Pred. No. 4.4e-103;
Matches 559; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

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BASE COUNT	246 a	197 c	214 g	349 t
Query Match	41.3%	Score 427.2;	DB 8;	Length 1006;
Best Local Similarity	73.6%;	Pred. No. 4.4e-103;		
Matches 559;	Conservative 0;	Mismatches 198;	Indels 3;	Gaps 1;
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QY	192	CATCTCAAGCAGGTTACCTTTACGCTATGCTGTCTTTAGTGGCATCGGCTCTCGGGCT	251	
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QY	252	TACCTTCACATCTATGAATATACGGTGGGCTCTCTCAACAAATGGCTTGCATGGGAGC	311	
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QY	312	ATGGTGTGGCTCTCTCAGCTCCCTTTATCAAGACGAAAAAGGCTGGCTCTCTCGATG	371	
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QY	372	GCAGCTGCACATTTTGAAGCGGCTCTATTGGTCTCTGATTGAGCTGGGCATTAACTTC	431	
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DB	448	GCAGCAGCAATGTTATSCAAGACGAGGAGATCTCTTACCTTCGAGACATGCTTTTCATCT	507	
QY	552	GGCGTCTCCCTCTCTTCTGTTGTGACATTTGCATCTCCATTTTGGTGGTCCCATGGCT	611	
DB	508	GGTTGTCTATGCTAATGTGGCTCCAGTTTGGCTCTTCAATCTTTGGTGGCTCTGCACT	567	
QY	612	GTTTTCAAGTTTGAATGTATTTTGGACCTTGTGTGTTTGTGGGCTACATCGTCTTGAC	671	
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Best Local Similarity 71.4%; Pred: NO. 1.3e-95;  
Matches 540; Conservative 0; Mismatches 213; Indels 3; Gaps 17

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Db	214	CTTACCTCCAGTCTCTCGAAATCATGGTGTATCTCACACCATTCATGTTTGGAA	273
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Db	274	CCATGATTGGCTTCTCTCATGTCTCTTATGAGCAACAAAGAGGCTCTCACTTCTCT	333
QY	370	TGGCAGCTGCATTTTTTGAAGGGCGCTCTATTGGTCTCTGATTGAGCTGGGCATTAAT	429
Db	334	TCCTCTCTGCGCTTCTTGAAGGTGCCTCTGTTGGCCCTTGATCAAGTGGCTGTGATT	393
QY	430	TGATCTCAAGCATGTGTTTGGCGCTTTTGTAGTGTGCTGTGGTTTTGGTTCCTTCT	489
Db	394	TTGACCCAAGCATCCTTATCACTGCGTTTGTGGAATCGATAGCGTTTATCTGTCTT	453
QY	490	CAGCTGTGCTCATGTTCGGCAGGCGCAGGAGTACTGTACTCTCGGGGCTCTCTTTCAT	549
Db	454	CAGGAGCAGCATGTGTCGACAGCAGAGATCTCTACCTCGGAGGACTCTCTCTT	513
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Db	514	CTGGCTTCTCATGCTTATGTGGCTTCAGTTTCCTTCTTCCATCTTTGGTGGCTCGGT	573
QY	610	CTGTTTTCAAAGTTTGAGTTGATTTTGGCATCTCTGGTGTTTTGGGCTACATCGTCTTG	669
Db	574	CCATCTTTAAGTTTGAGCTCTACTTTGGACTCTTGATCTTTGTTGGATACATGGTGTGG	633
QY	670	ACACCAAGAAATTTATGAGAGCTCCTCATCTGGGTGATATGATTTAGTTAAGCATGCAT	729
Db	634	ACACAAGAGATTTATAGAGAAACACACCTAGGGACATGGACTATGTGAACATGCAT	693
QY	730	TGACCCCTTTACAGATTTTGGCGCTCTTTTGTGGGATCTCTGATCATCATGTTTAAAGA	789
Db	694	TGACCCCTTTACCGAATTTGTGGCTGTGTTTGTCCGTGTTCTCATCAATATGCTGAAGA	753
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RESULT 10  
LOCUS AB025926 1181 bp mRNA linear PLN 04-MAR-2000  
DEFINITION Oryza sativa BI-1 mRNA for Bax inhibitor-1, complete cds.  
ACCESSION AB025926  
VERSION AB025926.3 GI:7209771  
KEYWORDS Bax inhibitor-1.  
SOURCE Oryza sativa (strain:Yamahoushi) cDNA to mRNA.  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Kawai.M., Pan.L., Reed,J.C. and Uchimiya.H.  
AUTHORS Evolutionally conserved plant homologue of the Bax inhibitor-1  
TITLE (BI-1) gene capable of suppressing Bax-induced cell death in yeast (1)

Kawai, M., Pan, L., Reed, J. C. and Uchimiya, H.  
Evolutionally conserved plant homologue of the Bax inhibitor-1  
(BI-1) gene capable of suppressing Bax-induced cell death in  
yeast (1)

PERS Lett. 464 (3), 143-147 (1999)  
 2006876  
 2 (bases 1 to 1181)  
 Kawai.M. and Uchimiya.H.  
 Direct Submission  
 Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,  
 Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,  
 Bunkyo-ku, Tokyo 113-0032, Japan  
 (E-mail: uchimiya@mbnbs.tam.u-tokyo.ac.jp, Tel:81-3-3812-2910,  
 Fax:81-3-3812-2910)  
 On Mar 8, 2000 this sequence version replaced gi:6759252.  
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 DB 166 CGCGAGCGCTGGGCTACGACTCGCTGAAGAACTTCGCCAGATCTCCCCGGCGTCC 225  
 QY 187 AATCTATCTCAAGCAGGTGTACTTACGCTATGCTGTCTTTAGTGGCATCGGCTGTG 246  
 DB 226 AGTCCACCTCTACGCTCGTTTACCTGCACACTATGCTGCGCCCTGGCTCGCGCGTGG 285  
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 QY 367 TGATGGCAGCTGCACATTTTGAAGCGGCTCTATTGGTCTCTGATTGAGCTGGGCATTA 426  
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 DB 466 ACTTGACTCAAGCATTTCTCGTAAACAGCATTTGTGGAACTGCCCATTCATTTGGGTGT 525  
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 QY 547 CATCTGGCGTCTCCCTCTCTCTCTGGTGCACCTTTGCACTCTCAATTTTGTGTGTCA 606  
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Qy      223  GTGCTTTAGTGGCATCGCTGCTGGGCTTACCTTACATTTCTATGCAATATCGGTGGGC 282
Db      128  TTGACTGGCTCACTGCGCGTGGTCTTACTCAATGCTGCAATGCTGCAATCGCGGGA 187
Qy      283  TCCTCACAAACATGGCTGTGATGGAAGCAATGGTGGCTTCTCAGTCTCTCTATTC 342
Db      188  TGTGACAAATCTCGCTTGTGCGAACTATCGCTGATGTTCTCGGTGCCAGTCTATG 247
Qy      343  AAGAGCAAAAAGGCTGCTCTCTGATGCGAGTGCACATTTTGAAGCGCTCTATTC 402
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Qy      463  GTTGTGCTGTTTGGTGTCTCTCAGCTGCTGCCATGTTGGCAAGCGCAGGGAGT 522
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Qy      523  ACTTGTACTCGGGGCGCTCTTTCATCTGCGCTCTCCCTCTCTCTGTTGCACTTTG 582
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Qy      583  CATCTCTCAATTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db      488  TCAGTCTCATCTTTGGGCACTCTCTCTGCGAGCTTCACTTTGAGGTTTACTTTGGCT 547
Qy      643  TGGTGTGTTGGGCTACATGCTCTTTGACACCCCAAGAAATTTATGAGAAGGCTCACT 702
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Qy      703  GTGATATGATAGCTTAAGCATGCTGACCTTTTACAGATTTTGGCGCTGTTTGG 762
Db      608  GCGACATGGATACATCAAGCAGCGCTTACCCCTCTTACCGACTTGTGCGCTCTCG 667
Qy      763  TCGGATCTGATCATCATGTTAAGAAATGATCTGAGAAGGAGAGAGAGAGAGAGA 822
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Db      728  GGA 730

RESULT 12
LOCUS   G73645
DEFINITION RZ957F etiolated leaf tissue of rice Oryza sativa STS genomic clone
VERSION G73645
KEYWORDS STS.
SOURCE 1 GI:19697240
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 418)
Oryza sativa STS
McGouch,S.R.
Unpublished (2002)

REFERENCE
AUTHORS Contact: Susan R. McCouch
JOURNAL Cornell University
TITLE Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
COMMENT Tel: 6072550420

```

Fax: 6072556683  
 Email: srm4@cornell.edu  
 Primer A: M13 Universal Forward GTAAACGACGGCCAGT  
 Primer B: M13 Universal Reverse AACAGCTATGACCATG  
 STS size: 418  
 Protocol:

Template: 20-100ng  
 Primer: 5pmol each  
 DNTps: 40nmol  
 Taq polymerase: 5units  
 Total volume: 50ul

Buffer:  
 Tris-HCl: 100mM  
 KCl: 500mM  
 MgCl2: 15mM  
 Gelatin: 0.1%  
 PH: 8.3

This is a partial sequence of the RFLP clone named above that was mapped at Cornell University Plant Breeding Dept. and sequenced at the Genome Sequencing Center at Cold Spring Harbor Laboratory. This marker is located on rice chromosome 2. For citations and other related information concerning this probe, please refer to the Gramene database at <http://www.Gramene.org>.

#### FEATURES

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STS  
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 Best Local Similarity 65.2%; Pred No. 1.1e-36;  
 Matches 262; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy 372 GCAGCTGCACCTTTTGAAGGCGCTCTATTGGTCTCTGATGAGCTGGGCAATTAACCTC 431
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RESULT 15
LOCUS BC000916
DEFINITION Homo sapiens, testis enhanced gene transcript, clone MGC:5230
ACCESSION BC000916
VERSION BC000916.1 GI:13111818
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
  1 (bases 1 to 2609)
  Strausberg, R.
  Direct Submission
  Submitted (16-NOV-2000) National Institutes of Health, Mammalian
  Gene Collection (MGC), Cancer Genomics Office, National Cancer
  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
  USA
  NIH-MGC Project URL: http://mgc.nci.nih.gov
  Contact: MGC help desk
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Baylor College of Medicine Human Genome
  Sequencing Center
  Center code: BCM-HGSC
  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
  Contact: villalobos@bcm.tmc.edu
  Villalobon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
  A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
  Muzny, D.M., Gibbs, R.A.
  Clone distribution: MGC clone distribution information can be found
  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
  Series: IRAP Plate: 3 Row: K Column: 7
  This clone was selected for full length sequencing because it
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GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 08:47:18 ; Search time 284 Seconds  
(without alignments)  
8199.177 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	416.8	40.3	1066	21	Arabidopsis thalia
3	221.2	21.4	884	22	Testis Enhanced Ge
4	219.2	21.2	527	22	Testis Enhanced Ge
5	198.4	19.2	712	21	Arabidopsis thalia
6	128.8	12.5	873	22	Bovine mammary tis
7	125.2	12.1	2922	21	Lung cancer associ
8	122	11.8	2600	24	Human cDNA differe
9	122	11.8	2634	19	Bax inhibitor Bi-1

10	83.8	8.1	751	24	ABQ56073	Human ovarian anti
11	77	7.4	380	21	AAQ04218	Human secreted pro
12	74	7.2	595	24	AAQ59227	Human colon cancer
13	72	7.0	520	20	AAV86028	EST clone B15. H
14	68.4	6.6	689	24	ABQ60318	Human colon cancer
15	61	5.9	506	24	ABQ58023	Human colon cancer
16	57	5.5	202	19	AAV16142	Microsatellite mar
17	47.8	4.6	6741	21	AAAI0595	Gene encoding a su
18	46.8	4.5	638	23	ABV25317	Human prostate exp
19	43.8	4.2	3654	23	ABLI2508	Drosophila melanog
20	43.8	4.2	3775	23	ABLI2504	Drosophila melanog
21	42.6	4.1	1618	24	ABT04036	Human ovary specif
22	42.4	4.1	752	24	ABQ14854	Oligonucleotide fo
23	42.4	4.1	752	24	ABQ14855	Oligonucleotide fo
24	41.4	4.0	10710	24	ABLI2892	Human immune syste
25	41	4.0	5059	20	AAK84332	Stealth virus nucl
26	40.8	3.9	463	21	AAQ03759	Human secreted pro
27	40.8	3.9	2296	19	AAV20662	Barley D-hordein g
28	40.8	3.9	2380	22	AAF63380	Barley CDNA involv
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36	38.8	3.8	437	24	ABL63599	Breast cancer rela
37	38.8	3.8	6445	22	AAI58443	Human polynucleoti
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42	38.6	3.7	4590	22	AAH24085	Yeast AOD9604-asso
43	38.2	3.7	590	24	ABQ19606	Oligonucleotide fo
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45	38.2	3.7	9510	22	AA646438	Tumour suppressor

#### ALIGNMENTS

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01-AUG-2002 (first entry)  
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PR 29-OCT-1999; 99US-0162142.  
Query Match 40.3%; Score 416.8; DB 21; Length 1066;  
Best Local Similarity 73.6%; Pred. No. 1.4e-111;  
Matches 559; Conservative 0; Mismatches 197; Indels 4; Gaps 2;  
QY 72 AAGAGAGAGACATGAGGTTTCATCGTCTTCGACGCGCAATCTGCTCGC 131  
DB 34 AAAAAACGAAACATGATCGGTTCTTCCTTCGATTCTCAACCTG---GTAGC 90  
QY 132 AACCGCTGGATTGATGTTCTCAAAAACCTCCGCCAGATCTCACCTCTGCTTCAAACT 191  
DB 91 AGAAGCTGGAGTATGATCTCTTAAAAACTCCGTCAGATTTCTCCAGCGGTTTCAAT 150  
QY 192 CATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCGGCT 251  
DB 151 CATCTTAAACGGTTTATTGACCTTATGTTGCTCTTGTGGGCTGCTGCTTTGAGCT 210  
QY 252 TACCTTCACATTTCTATGGAATATCGGTGCGCTCTCTCAACAATGCTTGCANGGAGC 311  
DB 211 TACCTCCATGTGCTCTGGAATATCGGCGGTATTTCTACACGATTGGATGATTGGAAT 270  
QY 312 ATGCTGCTGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGCGGCTCTTCTGATG 371  
DB 271 ATGATTGGCTCCTTTTCATGTCCTCTTATGAACACCAAAAAGGCTTCTTCTGTTT 330  
QY 372 GCAGCTGCACATTTTGAAGCGGCTCTATTGCTCTCTGATTGAGCTGGGCAATTAACCTC 431  
DB 331 GCCTGCTGCTTCTTCAAGGTGCTTCTGTTGCCCTTGTATCAAAAGTGGCAATTGATGT 390  
QY 432 GATCCAGCAATGCTGTTGGCGCTTTTGTAGTGTGCTGCTGTTTGTGCTTCTCA 491  
DB 391 GACCCAAGCATCTTATCACTCGTTGTTGGAATGCG-GATACGTTTGTCTGTTCTCA 449  
QY 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGCTCTTCTTCACT 551  
DB 450 GCAGCAGCAATGTTAGCAAGCAGCGAGGAGTATCTACCTTGGAGGACTGCTTTCATCT 509  
QY 552 GCGCTCTCCCTCTCTCTGCTGCTGCTTGTGATCTCTCAATTTTGGTGGTTCATGCT 611  
DB 510 GCGTGTCTATGCTAATGCTGCTTGTGCTGCTTGTGCTTGTGCTGCTGCTGCT 569  
QY 612 GTTTTCAAGTTGAGTTGATTTTGTGACTCTTGTGCTTGTGCTGCTGCTGCTTGTGAC 671

DB 570 ATCTTTAAGTTTGAGTTGACTTGGATCTTTTGATCTTTTGGGATACATGGTGGTGCAC 629  
QY 672 ACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATATGATTAAGTATGATGATG 731  
DB 630 ACACAGAGATTATAGAAAAGGCACACCTCGGTGACATGACTATGTAACATTCGTTG 689  
QY 732 ACCCTTTTACAGATTTTGGCGTGTGTTTGTGGGATCTCTCATCATGTTAAAGAAAT 791  
DB 690 ACCCTTTTCACTGACTTTGAGCTGTGTTTGTGGATCTCTCATCATGTTTGAAGAAC 749  
QY 792 GCATCTGAGAAGGAAGAAGAAGAAGAAGAAGAGAGAAACT 831  
DB 750 TCAGCAGATAAAGAGAAGAAGAAGAAGAAGAAGAGAAACT 789  
RESULT 3  
AAF44782  
ID AAF44782 standard; cDNA; 884 BP.  
XX  
AC AAF44782;  
XX  
XX 27-MAR-2001 (first entry)  
XX  
XX Testis Enhanced Gene Transcript protein coding sequence #1.  
DE Cell death modulator; programmed cell death; PCD; apoptosis;  
XX forestry plant; ss.  
KW  
XX Pinus radiata.  
OS  
XX WO200075331-A1.  
XX  
XX PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000MO-NZ00086.  
XX  
XX 04-JUN-1999; 99US-0325932.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
PI Flinn B, Lasham A;  
XX  
XX WPI; 2001-061724/07.  
DR P-PSDB; AAB65755.  
XX  
PT Novel defender against cell death polynucleotide useful for modulating  
PT programmed cell death pathway and specific development pathways in  
PT forestry plant -  
XX  
PS Claim 1; Page 62; 142pp; English.  
XX  
XX The present invention relates to coding sequences (see AAF44740-F44840  
CC and AAF4843-F4844) and proteins (see AAB65714-B65814) involved in  
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
CC of the present invention are useful for modulating a PCD or cell death  
CC pathway and various developmental pathways in a forestry plant, by  
CC stably incorporating one of the present coding sequences into the genome  
CC of the forestry plant, where the coding sequence provides a PCD pathway  
CC that is not present in a native form of the forestry plant.  
XX  
XX Sequence 884 BP; 219 A; 165 C; 216 G; 284 T; 0 other;  
SQ  
Query Match 21.4%; Score 221.2; DB 22; Length 884;  
Best Local Similarity 60.6%; Pred. No. 2.6e-54;  
Matches 383; Conservative 0; Mismatches 243; Indels 6; Gaps 1;  
QY 203 GGTGTACTTACGCTATGCTGTGCTTTAGTGGCATCGCTGCTGGGCTTACCTTCACAT 262  
DB 4 GGTATTATTGCTGCTAGCTGTGCTTCCCTCGTAAACAGCAGCATCGGTGTTTATTGCTCT 63  
QY 263 TCTTGAATATCGGTGCTGCTTCTCAACAATGCTTGCATGCGAAGCATGCTGTGGCT 322

Db 64 TCTGTTGAATATGGAGGCTCTCACGGGGCTCGCTTGCATTGGTTCTGTAAATCGGGCT 123  
QY 323 TCTCTCAGCTCTCTCTT-----ATCAAGAGCAAAAAGGFTGGCTCTTCTGTATGGCAGC 376  
Db 124 CTTATCCGTCCTTACTCTCTCAACAATAGGGTAAGAGAGCTGGCTGCTCTCTGGCAGC 183  
QY 377 TGCACATTTTGAAGCGGCTCTATTGGTCTCTGATTGAGCTGGGCATTAACCTTCGATCC 436  
Db 184 TGTGTGGTTCAAGGAGCTACTCTGGACCGCTCATCGACGGTFCATATATTTGACTC 243  
QY 437 AAGCATGTGTGGCGCTTTTGTAGTTGTCTGCTGGTTTGTGGTTTGTCTCTCAGCTGC 496  
Db 244 CAGTATACTGGTGAAGTCTTTTGGGACCTCTTGGCCCTTCGCTTCTTTCGGCAGC 303  
QY 497 TGCATGTTGGCAAGCGCAGGAGTACTTGTACTTCGGGGCTTCTTTCATCTGGGT 556  
Db 304 AGCAATCACAGCAGAGAGAGGATACCTATTTTGGAGAGATTATTTGGCGCTGGGAT 363  
QY 557 CTCCTCTCTCTCTGCTTGCATTTGCACTTTCATCTCCCTCCATTTTGGTGGTTCATGGCTGTTT 616  
Db 364 CAGCATATTGATGGCTGCAACTAGCATCTCTCGATTTTGGTGGTCTTCTCGGCGATT 423  
QY 617 CRAAGTTGAGTTGATTTTGGACTCTTGGTGTCTTGGGCTACATCGTCTTGCACCCA 676  
Db 424 CACATTTGAGATCTCTCGCTCTGCTAGTTTCTTGGGTTATATATTTTGGACACA 483  
QY 677 AGAATATTGAGAGGCTCACTTGGGTGATATGGATTACGTTAAGCATGATTAACCT 736  
Db 484 GATGATCATCGAAGAGCGACCATGGAGACTATGATTATTTAAACATTCACCTGGACCT 543  
QY 737 TTTTCACAGATTTGGCGCTTTTCTGCGGATCTGATCATCATGTTTAAAGATGCATC 796  
Db 544 CTTGATGACTCTGCTGCTGTATTTCTTCCCTGATGGTCAATATGGCAAGAAATGCAGA 603  
QY 797 TGAAAGGAAGAGAGAAGAAAGAGAGAGAA 828  
Db 604 CAGTAAATCCAGGAGGAGGAGAAAGAGAA 635

## RESULT 4

AAP44783  
ID AAP44783 standard; cDNA; 527 BP.

AC AAP44783;

DT 27-MAR-2001 (first entry)

XX Testis Enhanced Gene Transcript protein coding sequence #2.

XX Cell death modulator; programmed cell death; PCD; apoptosis;

XX forestry plant; ss.

XX Pinus radiata.

XX WO200075331-A1.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-NZ00086.

XX 04-JUN-1999; 99US-0325932.

XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Flinn B, Lasham A;

XX WPI; 2001-061724/07.

XX P-PSDB; AAB65756.

XX Novel defender against cell death polynucleotide useful for modulating,  
XX programmed cell death pathway and specific development pathways in  
XX forestry plant ;

XX Claim 1; Pages 62-63; 142pp; English.

XX The present invention relates to coding sequences (see AAP44740-F44840  
and AAP44843-F44844) and proteins (see AAB65714-B65814) involved in  
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
CC of the present invention are useful for modulating a PCD or cell death  
CC pathway and various developmental pathways in a forestry plant, by  
CC stably incorporating one of the present coding sequences into the genome  
CC of the forestry plant, where the coding sequence provides a PCD pathway  
CC that is not present in a native form of the forestry plant.

XX Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;

Query Match 21.2%; Score 219.2; DB 22; Length 527;  
Best Local Similarity 74.5%; Pred. No. 7.7e-54;

Matches 289; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

QY 130 GCAACGGCTGGAGTTATGATTCTCTCAAAACTTCCGCCAGATCTCACCTCTCGTTCAAA 189

Db 141 GCAAGGGTGGAGCCAGATTCCCTCAAGAACTTCCGCCAGATATCTCCGCCCTCCAAAT 200

QY 190 CTCATCTCAAGCAGGTGTACTTACGCTATGCTGCTTGTAGTGGCATCGGCTCGGG 249

Db 201 CTCACCTCAAGAACTTTATCTGTCTTATGCTGTGCTTGAUGGCTTCGCCCGGTGGTG 260

QY 250 CTTACTCTCACATTTCTATGGAATATCGGTGGCTTCTCACAAATCGCTTGCATGGAA 309

Db 261 CTTACTCTCATCTGATGCTGAACATCGCGGGCTCTCACACAAATTCCTTGCATCGGAA 320

QY 310 GCATGGTGGCTTCTCTCAGCTCTCTCTTATCAAGACAAAGAGGCTGCTCTCTGA 369

Db 321 GCATGGTGGCTGCTCTCTGATTTCTCCACATGAAGAGCAAAAGAGTTTGGTCTGTCA 380

QY 370 TGGCAGCTGCACCTTTTGAAGCGCTCTATTGGTCTCTGATTTGAGCTGGGCATTAACT 429

Db 381 TGGCGCGCTCTCTTTGAAGGAGCGTGTATCGGTCTCTCATCGAAGCGCCATTAAAG 440

QY 430 TCGATCCAGCATTTGTTGGCGCTTTTGTAGTTGTGCTGTGTTTGGTGGCTTCT 489

Db 441 TCGAOCGAGCATTTGTGATAGCGCATTTGTGGGATCTGCGCTGCGCTTCGCTTGTCTTCT 500

QY 490 CAGCTGCTGCCATTTTGGCAAGCGCGAG 517

Db 501 CGGGCGCAG-CATGTTGGCTAGCGGAG 527

## RESULT 5

AAC51940

ID AAC51940 standard; DNA; 712 BP.

XX AAC51940;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 70058.

XX Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.



PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140931.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0143977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0148568.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 28-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151067.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 28-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.

PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
PR	13-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	14-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160766.	
PR	21-OCT-1999;	99US-0160770.	
PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161932.	
PR	28-OCT-1999;	99US-0161933.	
PR	29-OCT-1999;	99US-0162142.	

Query Match 19.28; Score 198.4; DB 21; Length 712;  
 Best Local Similarity 70.9%; Pred. No. 1.1e-47;  
 Matches 278; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

OY	72	ARGAGAGAGAACAAATGGAGAGTTTACATCGTTCTTCGACTCGCAATCGCTCTCGC	131
DB	25	AAAAAAACGAACAAATGGATGCGTTCTTCTCTTCTTCGATTCTCAACCTG---GTAGC	81
OY	132	AACCGTGGAGTATGATTCTCATAAACTTCGCGCAGATCTCACTCTCGTCAAAC	191
DB	82	AGNAGCTGGAGTATGATTCTTAAAACTTCGTCAGATTCTCGACCGTTCAAGAT	141
OY	192	CATCTCAACACAGGTGTAACGTATGCTGTCGTTAGTGGCATCGGCTCTGGGCT	251
DB	142	CATCTTAAACGGGTTTATTGACCTTATGTTGTCTCTTCTTGGCGCTCGCTTTGGAGCT	201
OY	252	TACCTTCACATCTTATGGAATATCGTGGCGCTCTCTCAACAATGCTTGCATGGGAAGC	311
DB	202	TACCTCCATGCTCTGGAATATCGCGGTATCTTCAACAGATTGAGTATGGAAT	261
OY	312	ATGGTGTGCTTCTCTCAGCTCTCTTATPACAGAGCAAAAAGGTGGCTCTTCTGATG	371
DB	262	ATGATTGGCTCTTCTCATGCTCTCTTATGAACACCAAAAAGGCTTTCTCTCTGTTT	321
OY	372	GCAGCTGCATTTTGAAGGCGCTCTATGGTCTCTGATTGAGCTGGGCATTAACTTC	431
DB	322	GCCTGCTGCTTCTTGAAGGTGCTTCTGTGGCGCTTGTATCAAGTGGCAATTGATTT	381
OY	432	GATCCAAGCATGTGTTTGGCGCTTTTGTAGG	463
DB	382	GACCCAGCATCTTATCACTACGCTGTTGTTGG	413

RESULT 6  
 AAF92293  
 ID AAF92293 standard; cDNA; 873 BP.  
 XX  
 XX AAF92293;  
 XX  
 XX  
 XX  
 XX 15-MAY-2001 (first entry)  
 XX  
 XX Bovine mammary tissue derived cDNA #6.

XX Bovine; mammary gland; cancer; tumour; angiogenesis; ss.  
 KW Bos taurus.  
 XX WO200114553-A1.  
 OS 01-WAR-2001.  
 XX PD  
 XX 23-AUG-2000; 2000WO-NZ00166.  
 XX 23-AUG-1999; 99US-0150330.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 XX (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
 PA Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;  
 PI WPI; 2001-226619/23.  
 XX  
 XX New polypeptides and polynucleotides encoding the polypeptides, which  
 PT are expressed in bovine mammary gland tissue, useful for stimulating  
 PT mammary gland growth or function, or inducing differentiation of milk  
 PT producing cells -  
 XX  
 XX Claim 1; Page 43; 97pp; English.  
 XX  
 XX The present invention relates to proteins derived from bovine  
 CC mammary gland cells, the invention is useful for stimulating the  
 CC bovine mammary gland cell growth and function, inhibiting the  
 CC growth of various mammary gland cancer cells, inhibiting  
 CC angiogenesis and vascularization of tumours, or modulating  
 CC the growth of blood vessels in a mammal.  
 XX  
 XX Sequence 873 BP; 206 A; 218 C; 196 G; 253 T; 0 other;  
 SQ

Query Match 12.5%; Score 128.8; DB 22; Length 873;  
 Best Local Similarity 52.5%; Pred. No. 3.1e-27;  
 Matches 386; Conservative 0; Mismatches 328; Indels 21; Gaps

QY 144 TATGATTCTCTCAAAAACCTCCGCGACATCTCACCTCTCGTTCAAACATCATCTCAAGCAG 203  
 DB 58 TTGTATGACTCTTTAAATTTCCACATAAACCCCTGCACACGACGACCTTGAGAG 117

QY 204 GTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTGGGGCTTACCTTCA---- 259  
 DB 118 GTTATGCGAGTTTGGCCCTCTGTATGTTTGTGCGCGCTCGGGGGCTTATATCCATGTG 177

QY 260 --CATTCTATGGAATATCGGNGGCTCCTCACAAATGGCTTGATGGAAGAGCATGTG 317  
 DB 178 GTACCCATTCATTACGGCTGGCGTCTCTCTGCTTGGGCTCTTTGGGGTTGAAT 237

QY 318 TGGCTTCTCTACGCTCTCTCTTATCAAG-----AGCAAAAAGGGTGGCTCTTCTGTAG 371  
 DB 238 TGGCTGATGGCAACACCTTCACGCAATGAACACTGACAAAAGACTTGGGACTTCTGGCT 297

QY 372 GCAGCTGCACATTTTGAAGGCGCTCTATTGGTCCCTGATTTGAGCTGGGCAATCACTTC 431  
 DB 298 GGAATTTGCTTTCCTTACAGGAGTTGGCGCTGGGGCCCTGCTCTGGACTTTGGCATGCCATC 357

QY 432 GATCAAGACATGTGTTTGGCGCTTTTGTAGTTGTGCTGTGTGTTTTTGGTTGCTTCTCA 491  
 DB 358 AACCCAGATCCTTCCCACTGCTTTCATGCGCACAGCAATGATCTTCACTGCTTCACC 417

QY 492 GCTGTGCCAATTTGGCAAGCGCAGGGAAGTACTTGTAACTCGGGGGCTCTCTTCACT 551  
 DB 418 CTGAGTGCACCTATGCGCAGCGCGTAGTACCTCTTTCTAGGAGGTATCTGTAGTGC 477

QY 552 GCGGTCTCCCTTCTCTTCTGGTTGCACTTTTGCATCTCCATTTTGGTGGTTCATGGCT 611  
 DB 478 GCAATGAGCCTCATGCTCTGTCTTCCCTGG---GGAACTTTTCTTCGATCTGTTGG 534

QY 612 GTTTTCAAGTTTGAAGTTGTAATTTTGGACTCTTGGTGTGTGTGGGCTACATCGTCTGAC 671

535 CTTTCCAGGCAACCTGTATATGGGCTGGTGGTCAATGTGGCTTTCTCTTTTGGAT 594  
672 ACCCAAGAAATTATGAGAGGCTCACTTGGGATGATGATTAAGCATGATTG 731  
595 ACTCACTCAATTATGAAAGGCTGAATGAGATTAAGATTAATCTGGCCTGCTT 654  
732 ACCCTTTACAGATTTGGCGCTGTTTTGCGGATCTGATCATGATGTTAAAGAT 791  
655 GACCTCTCTTGGATTCGTAACCTCTCTCAGAAAGCTCATGATGATCTGGCTATGAT 714  
792 GCATCTGAGAGGAG 851  
715 G-----AGAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768  
852 GGTTCANAACTCC 866  
769 ACTTCTCTCCCTCC 783

RESULT 7  
AAF18054  
ID AAF18054 standard; DNA; 2922 BP.  
XX AC AAF18054;  
XX DT 14-MAR-2001 (first entry)  
XX DE Lung cancer associated polynucleotide sequence SEQ ID 73.  
XX KW Human; lung cancer associated protein; neuroprotective; cytostatic;  
KW cardioactive; immunomodulatory; muscular active; vulnary;  
KW gastrointestinal; nephrotropic; antiinfective; gynecological;  
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
KW proliferative disorder; wound healing; infectious disease; ds.  
XX OS Homo sapiens.  
XX PN WO200055180-A2.  
XX PD 21-SEP-2000.  
XX PF 08-MAR-2000; 2000WO-US05918.  
XX PR 12-MAR-1999; 99US-0124270.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (ROSE/) ROSEN C A.  
XX PI Ruben SM;  
XX DR WPI; 2000-587514/55.  
XX DR P-PSDB; AAB58178.  
XX PT Lung cancer associated gene sequences, referred to as lung cancer  
XX PT antigens, useful for treatment, prevention, and diagnosis of disorders  
XX PT such as lung cancer -  
XX PS Claim 1; Page 550-551; 1425pp; English.

CC Polynucleotide sequences AAF17992 - AAF18424 encode human lung cancer  
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer  
CC associated proteins and polynucleotide sequences, their agonists, and  
CC antagonists may have neuroprotective; cytostatic; cardioactive;  
CC immunomodulatory; muscular active general; vulnary; gastrointestinal  
CC general; nephrotropic; antiinfective; gynecological; or antibacterial  
CC activity. The invention also includes antibodies specific for the  
CC protein or polynucleotide sequences. The lung cancer associated  
CC polynucleotide sequences may be used for detection of lung cancer,  
CC chromosome identification, as chromosome markers, and for numerous other  
CC diagnostic or research purposes. The proteins may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

disorders. The proteins may also be used in the treatment of wounds and  
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
CC peptide AAB58549 are used in the course of the invention for the  
CC identification and characterisation of the polynucleotide and protein  
CC sequences.  
XX  
SQ Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;  
Query Match 12.1%; Score 125.2; DB 21; Length 2922;  
Best Local Similarity 52.2%; Pred. No. 6.5e-26;  
Matches 358; Conservative 0; Mismatches 313; Indels 15; Gaps 3;  
QY 144 TATGATCTCTCAAAACCTTCGCCAGATCTCACCTCTCGTTCAAACCTCATCTCAAGCAG 203  
DB 141 TTTGATGCGCTTTTAAATTTTCTCATATAACCCGTCACACGACGACACCTGAGAAG 200  
QY 204 GTGTACTTAACGATATGCTGCTTTAGTGGCAATGCGCTGCTGGGCTTACCTTCA---- 259  
DB 201 GTCTATGCAAGTTTTGCCCTTTGTATGTTGTGGCGGCTGCAGGGGCTATGTCCATATG 260  
QY 260 --CATTTCTATGGAATATCGTGGCTCTCTCAACAATGCTTGTATGGGAAGCATGCTG 317  
DB 261 GTCACTCATTTTATTCAGGCTGGCTGTCTGTCTGCTTGGGCTCCCTGATATTGATGATT 320  
QY 318 TGGCTTCTCTCAGCTCCTCTTATCAAGAG-----CAAAAAAGSGTGGCTCTTCTGATG 371  
DB 321 TGGCTGATGGCAACACCTCATAGCCATGAACCTGAACAGAAAGACTGGGACTTCTTGTCT 380  
QY 372 GCAGCTGCATTTTGAAGCGCCTTATTTGCTCTCTGATTTGAGCTGGCATTAACCTTC 431  
DB 381 GGATTTGATCTTCTTACAGAGATGGCTGGGCCCTGGCTGGAGTTTGTATTGCTGTC 440  
QY 432 GATCCAGCAATGTTGTTGGCGCTTTTGTAGTTGTGCTGTGGTTTTTGGTGTCTTCTCA 491  
DB 441 AATCCAGCACTCTTCCCACTGTTTTCATGGCAGCGCAATGATCTTTACCTGCTTACC 500  
QY 492 GCTGCTGCCATGTTGCAAGGCGGAGGAGTACTTGTACTCGGGGCTCTTCTTCACT 551  
DB 501 CTAGTGCACTCTATGCCAGGCGCCCTAGCTACCTCTTCTGGGAGGTATCTTGATGTC 560  
QY 552 GGGCTCTCCCTCTCTTCTTGGTTGCACTTTGCACTCTCTCAATTTTGGTGGTTCACGCT 611  
DB 561 GCCCTGAGCTGTGTTGCTTTGCTTCTCCCTGGGGAAT--GTTTTCTTGGATTCACATTGG 617  
QY 612 GTTTTCAAGTTTGAGTTGATTTTGGACTCTTGGCTTTGTGGCTACATGCTCTTTTCAC 671  
DB 618 CTTTTCAGGCAAAACCTGTATGAGGACTGGTGGTCAATGCTGTGGCTTCTGCTTTTGTAT 677  
QY 672 ACCCAAGAAATTATGAGAGGCTCACTTGGGTGATGATGATTACGTTAAGCATGCAATG 731  
DB 678 ACTCACTCATTTTGAAGAGGCGGCAACATGAGATCAAGATTATATCTGGCAGCTGCATT 737  
QY 732 ACCCTTTTCAAGATTTTGGCGCTGTTTGTGGGATCTCTGATCATCATGTTAAAGAT 791  
DB 738 GATCTCTTCTTAGATTTTCACTTACTGCTTTCAGAAACTCATGATGATCTGCGCATGAT 797  
QY 792 GCATCTGAGAGAGAGAGAGAGAGAA 817  
DB 798 GAAAGGATTAAGAGAGAGAGAGAA 823

RESULT 8  
ABK84658  
ID ABK84658 standard; cDNA; 2600 BP.  
XX AC ABK84658;  
XX DT 14-AUG-2002 (first entry)  
XX DE Human cDNA differentially expressed in granulocytic cells #1229.  
XX DE Human; ss; granulocytic cell; DNA chip; bacterial infection;  
XX KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 DR WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity -

XX Claim 1; SEQ ID No 1229; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) Gs by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating Gs; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease; also bacterial infection, viral infection,  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other;

XX Query Match 11.8%; Score 122; DB 24; Length 2600;

XX Best Local Similarity 51.9%; Pred. No. 5.3e-25;

XX Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;

QY 144 TATGATCTCTCAAAAACTCCGCCAGATCTCACTCTCGTTCAAACTCATCTCAAGCAG 203  
 Db 68 TTTCATGCGCTTTTAAATTTTCTCATATAAACCCTCAACGACAGCAGCAGCAG 127  
 QY 204 GTCTACCTTACGCTATGCTGCTTTAGTGGCATCGGCTGCTGGGGCTTACCTTCA--- 259  
 Db 128 GTCTATGCGAAGTTTTCCTTTTGTATGTTTGGGGCTGCGAGGGCTATGTCATATG 187  
 QY 260 --CATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGT 317  
 Db 188 GTCACTCAATTCATTGAGGCTGGCTGCTGTCTGCTGGGCTCCCTGATATTGATGAT 247  
 QY 318 TGGCTTCTCTCAGCTCCTCTTATCAAGAG-----CAAAAAAGGGTGGCTCTCTCTGATG 371  
 Db 248 TGGCTGATGGCAACCTCTATAGCCATGAACCTGAACAGAAAGACTGGACTTCTTGCT 307  
 QY 372 GCAGCTGCACATTTTGAAGGCGCTTATTTGGTCTCTCTGATTTGAGCTGGGCAATTAACATTC 431  
 Db 308 GGATTTGCATTTCTACAGGAGTGGGCTGGGCGCTGCGCTGGAGTTTTTGTATTGCTGTC 367  
 QY 432 GATCCAGCATTTGTTGGCGCTTTTGTAGTTGTCTGTGGTTTGGTTGGTCTCTCA 491  
 Db 368 AACCCAGCATCTCTCCCACTGCTTTTCATGGGCACAGCAATGATCTTTACCTGCTTACC 427  
 QY 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTTGTACCTCGGGGGCTTCTTTTCATCT 551  
 Db 428 CTCAGTGCACCTCTATGCCAGGCGCTAGCTACCTCTTTCGGGAGGTATCTTGATGTCA 487  
 QY 552 GGGCTCTCCCTCTCTCTGTTGGTGCACCTTGCATCTCTCCATTTTGGTGGTCCATGGCT 611  
 Db 488 GCGCTGAGCTTGTGTTTTGTTCTTCCCTGGGGAAT---GTTTTCTTTGGATCCATTGG 544  
 QY 612 GTTTTCAAGTTTGAGTTGATTTTGGACTCTTTGGTGTGTTGGGCTACATCGTCTTTTGAC 671  
 Db 545 CTTTCCAGGCAACCTGATGTTGGGACTTGGTGGTCTGTTGGCTTCGTTCTTCTTGAT 604  
 QY 672 ACCCAAGAATATTGAGAAGGCTCATTGGGTGATGATGATGATGATGATGATGATGATG 731  
 Db 605 ACTCAACTCATTTATTTAAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCAGCTGCAT 664  
 QY 732 ACCCTTTTACAGATTTTGGCGCTGTTTTTGTGGGATTCTGATCATCATGATTAAAGAAAT 791  
 Db 665 GATCTCTCTTAGATTTTCACTACTGTTCTTCAGAAACTCATGATGATGATGATGATGAT 724  
 QY 792 GCATCTGAGAAGGAAGAAGAAAGAA 817  
 Db 725 GAAAAGGATAAGAAGAAGAAGAAGAA 750

# RESULT 9

AAV59067

ID AAV59067 standard; cDNA; 2634 BP.

XX

XX AAV59067;

XX

DT 02-FEB-1999 (first entry)

XX

DE Bax inhibitor BI-1 cDNA.

XX

KW Bax inhibitor; BI-1; human; apoptosis; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 73..786

FT /\*tag= a

XX

PN WO9840397-A1.

XX

PD 17-SEP-1998.

XX

PF 13-MAR-1998; 98WC-US05015.

XX

PR 14-MAR-1997; 97US-0818514.  
XX (BURN-) BURNHAM INST.  
PA Reed JC, Xu Q;  
XX WPI; 1998-531519/45.  
DR P-PSDB; AAW73136.  
XX  
PT Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate  
cellular apoptotic activity or identify agents altering BI-1 or BI-2  
binding which can modulate apoptotic activity  
XX  
PS Claim 2; Page 61-63; 80pp; English.  
XX  
CC This cDNA clone codes for an inhibitor protein, termed BI-1 (see  
AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding  
BI-1 and BI-2 (see AAW59068) were identified by suppression of  
CC Bax-induced death of yeast cells transformed to express human Bax.  
CC A human HepG2 cDNA library was used for library screening. The  
CC invention provides vectors, optionally expression or viral vectors,  
containing BI nucleic acids, and host cells containing these  
CC vectors. The nucleic acids encoding BI-1/BI-2 can be used to  
increase expression of these proteins in cells, or antisense  
CC molecules prepared from them used to decrease expression. In  
these ways, cellular apoptotic activity may be modulated (claimed).  
CC The nucleic acids and complementary sequences are also useful as  
probes to detect BI-encoding nucleic acid molecules in samples.  
XX  
SQ Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;  
Query Match 11.8%; Score 122; DB 19; Length 2634;  
Best Local Similarity 51.9%; Pred. No. 5.4e-25;  
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;  
QY 144 TATGATTTCTCAAAACCTTCGGCCAGATCTCACCTCTGTTCAAACTCATCTCAAGCAG 203  
DB 100 TTGATGCGCTTTTAAATTTCTCATATAACCCCGTCAACGACGACGACCTGAAGAAG 159  
QY 204 GTGATCTTACGCTATGCTGTCTTTAGTGCATCGCTGCTGGGCTTACCTTCA ---- 259  
DB 160 GTCATGCAAGTTTTCCTTTGATGTTGTTGGCGCTGCAGGGGCTATGTCATATG 219  
QY 260 --CATCTATGGAATATCGTGGCTCTCTCAACAATGCTTGCATGGGAACATGGTG 317  
DB 220 GTCACATATTCATTACAGCTGGGCTGTCTGCTGGGCTCCCTGATTTGATGATG 279  
QY 318 TGGCTTCTCTAGCTCCCTCTTATCAAGAG-----CAAAAAGGGTGGCTCTTCTGATG 371  
DB 280 TGCTGATGCGCAACCTCATAGCATGAACCTGAACAGAAACAACTGGGACTTCTTGCT 339  
QY 372 GCAGCTGCACATTTTGAAGGCGCTCTATTGCTCTGATTGAGCTGGGCATTAATTC 431  
DB 340 GGATTTGCAATCTTACAGGAATTGGGCTGGGCGCTGCCCTGGAGTTTGTATGCTGTC 399  
QY 432 GATCAAGCATTTGTTGGGCGCTTTTGTAGTGTGTGCTGTTGTTTGTGTTCTCA 491  
DB 400 AACCCAGCATCTTCCACATGCTTTTATGCGCAGCGCAATGATCTTTACTGCTTCA 459  
QY 492 GCTGTCGCATTTTGGCAAGGCGAGGAGTACTGTACCTCGGGGCTTCTTCACT 551  
DB 460 CTCAGTGCATCTATGCCAGGCGCGGTAGTACCTCTTCTGGGAGGTATCTTGAATCA 519  
QY 552 GGCGTCTCCTCTCTCTGTTGTGACATTTGATCTCCATTTTGTGTTTCCATGGCT 611  
DB 520 GCGCTGAGTGTGCTTTTGTCTTCCCTGGGAT---GTTTCTTTGATCATTTGG 576  
QY 612 GTTTTCAAGTTGAGTTGATTTGAGCTCTTGGTGTGTTGGCTACATGCTTTGAC 671  
DB 577 CTTTTCAGGCAACCTGTATGAGGAGTGTGGTGTGCTGCTGCTTTTGTAT 636  
QY 672 ACCAAGAAATATTGAGAGGCTCACTTGGGTGATATGATTTAGCTTAACATGATG 731

DB 637 ACTCAACTCATTTGAAAAGGCGCAACATGAGATCAAGATTATATCTGGCACTGCATT 696  
QY 732 ACCCTTTTACAGATTTTGGCGCTCTTTTGTGGGATTCATCATCATCTTTAAAGAT 791  
DB 697 GATCTCTTCTTGAATTTTCAATCTGCTTCAAAAACCTCATGATGATCTGGCCATGAAT 756  
QY 792 GCATCTGAGAGGAGAGAGAGAGAA 817  
DB 757 GAAAGGATAAGAGAGAGAGAGAA 782  
RESULT 10  
ABQ56073  
ID ABQ56073 standard; cDNA; 751 BP.  
XX  
AC ABQ56073;  
DT 22-AUG-2002 (first entry)  
DE Human ovarian antigen HPDWT56 cDNA, SEQ ID NO:1953.  
XX  
KW Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
ovarian cancer; breast cancer; tumour; reproductive system disorder;  
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
inflammatory condition; immune disorder; blood disorder;  
cardiovascular disorder; respiratory disorder; neurological disorder;  
gastrointestinal disorder; urinary system disorder; drug screening;  
gene therapy; chromosome mapping; forensic analysis;  
antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
antiinflammatory; gynaecological; reproductive; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
EF 07-JUN-2001; 2001WO-US18569.  
XX  
PR 07-JUN-2000; 2000US-209467P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
XX  
DR WPI; 2002-147878/19.  
DR P-PSDB; ABP42996.  
XX  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
useful in the prevention, treatment and diagnosis of cancer (e.g.  
ovarian cancer), immune disorders, cardiovascular disorders and  
neurological diseases.  
PS Claim 1; SEQ ID NO 1953; 2922pp; English.  
XX  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
encompasses polypeptides 90% identical and polynucleotides 95% identical  
to the sequences of the invention. The invention additionally relates to  
recombinant vectors and host cells comprising human ovarian antigen  
polynucleotides, antibodies against human ovarian antigens, and the use  
of ovarian antigen polynucleotides and polypeptides in diagnosing,  
treating, prognosing or preventing various ovary and/or breast-related  
disorders. Such conditions include ovarian cancer and breast cancer, and  
metastatic tumours of ovarian or breast origin, reproductive system  
disorders (e.g., infertility, disorders of pregnancy, anovulation,  
polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic  
shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
vaginitis), immune disorders (e.g., congenital and acquired  
immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents cDNA encoding a human ovarian antigen of the  
CC invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;

Query Match 8.1%; Score 83.8; DB 24; Length 751;  
Best Local Similarity 50.6%; Pred. No. 4.3e-14;  
Matches 312; Conservative 0; Mismatches 288; Indels 16; Gaps 4;

QY 144 TATGATCTCTCAAAACTTCGCGAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG 203  
Db 93 TTGATGCGCTTTAAATTTCTCATATAACCCGTCACGACGACACCTCGAAGAG 152  
QY 204 GTGACCTTAGCTAGCTGTCTTATGAGGATCGGCTGCTGGGGCTTACCTTCA---- 259  
Db 153 GTCTATGCAAGTTTTCGCTTTGTATGTTGTGGCGGCTGCGAGGCGCTATGTCCATATG 212  
QY 260 --CATCTATGGAATATCGTGGCTCCCTCACAACTGCTTGCATGGGAGCATGGTG 317  
Db 213 GTCACTCATTTATTCAGCTGGCTGCTGCTGCTGGCTCCCTCATATTGATGATT 272  
QY 318 TGCGTCTCTAGCTCTCTCTATCAAGAG-----CAAAAGGGTGGCTTCTGTATG 371  
Db 273 TGGCTGATGCAACACCTCATAGCCATGAACGAAAGAACTGGGACTTCTTGCT 332  
QY 372 GCAGCTGCATTTTGAAGCGCTCTATTGCTCTGATTTGAGCTGGGCAATTAACCTC 431  
Db 333 GAATTTGCATCTCTACAGAGTGGCTGGCGCTGCGCTGAGTTTGTATGCTGTC 392  
QY 432 GATCCAGCATTTGTTGGCGCTTTTGTAGGTTGCTGCTGGTTTTGGTTGCTCTCA 491  
Db 393 AACCCAGCATCTCTCCCACTGCTTTCATGGGCAAGCAATGATCTTTACCTGCTTACC 452  
QY 492 GTGCTGCCATGTTGCAGGCGCAGGAGTACTGTACTCGGGGCTTCTTTCATCT 551  
Db 453 CTGAGTGCACTCTATGCCAGGCGCCGAGTACTCTTTCTGGGAGGTATCTGTATGTC 512  
QY 552 GGGCTCTCCCTTCTCTCTGTTGCACTTTGCACTCTCCATTTTGGTGGTTCCATGGCT 611  
Db 513 AGCCTGAGCTTGGTGTCTTGTCTCCCTGG---GGAATGGTTTCTTTGGATCCATTGG 569  
QY 612 GTTTTCAAGTTTGAATTTTGGACTCTTGGTTTGTGGCTACATCGTCTTTGAC 671  
Db 570 CTTTTCAGGCAACCTGTATNTGGGACTGGTGGTCACTGTGGCTTC-GCCTTTTGTAT 628  
QY 672 ACCCAAGAAATTTAGAGAGGCTCACTTGGTGTATATGGATTAAGCATGCAATG 731  
Db 629 ACTCACTCATTTGAAGAGCGGACATGGAGATCAAGATTATATCTGGCACTGCAATT 688  
QY 732 ACCCTTTTCAAGATT 747  
Db 689 GATCTCTTTAAGATT 704

RESULT 11  
AAC04218  
ID AAC04218 standard; cDNA; 380 BP.  
XX  
AC AAC04218;  
XX AC  
XX AC  
DT 06-OCT-2000 (first entry)  
XX

DE Human secreted protein 5' EST, SEQ ID NO: 8293.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
XX Gene therapy; chromosome mapping; ss.  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-0200610.  
XX  
PR 26-FEB-1999; 99US-0122487.  
XX  
PA (GSEST) GENSET.  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
PS Claim 1; SEQ ID 8293; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.

XX  
SQ Sequence 380 BP; 88 A; 88 C; 81 G; 121 T; 2 other;  
Query Match 7.4%; Score 77; DB 21; Length 380;  
Best Local Similarity 53.7%; Pred. No. 3e-12;  
Matches 180; Conservative 1; Mismatches 151; Indels 3; Gaps 1;

QY 483 TGGTTCTAGCTGCTGCCATGTTGCAAGGCGGAGGAGTACTGTACCTCGGGGCTT 542  
Db 2 TGGTTCACTCAGTGCACTCTATGCCAGGCGCGGTAGCTACCTCTTCTGGGAGGTATC 61  
QY 543 CTTTTCATCGGGTCTCCCTTCTCTCTGTTGCACTTTGCATCTCCATTTTGGTGGT 602  
Db 62 TTGATGTGACCTCAGCTTGTGCTTTTGTCTTCCCTGG---GGAATGTTTCTTTTGA 118  
QY 603 TCCATGGCTGTTTCAAGTTTGAAGTTGATTTTGGACTCTTGGTGGTTGGGCTATC 662  
Db 119 TCCATTTGGCTTTTCCAGGCAACCTGTATGTGGGACTGGTGGTCAATGTGGCTTGGT 178  
QY 663 GTCTTTGACACCCCAAGAAATTTTGAAGAGGCTCACTGGGTGATATGATTAAGTTAAG 722  
Db 179 CTTTGTGATCTCACTCATTTATTTGAAGGCGGACATGGGATCAAGATTATATCTGG 238  
QY 723 CATGCAATTAACCTTTTTCACAGATTTTGGCGCTGTTTTTGGCGGATTTCTGATCATG 782  
Db 239 CACTGCAATGATCTCTTCTTAGATTTTCAATTTCTGTTCTCAGAAAACTCATGATGCTG 298  
QY 783 TTAAGAAATGCACTCTGAGAGGAGGAGAGAGAGAA 817  
Db 299 GCCATGATGAAGAGGATGAAGAGAGAGAGAGAA 333

RESULT 12  
ABO59227/c  
ID ABO59227 standard; cDNA; 595 BP.  
XX AC ABO59227;  
XX AC ABO59227;  
XX DT 02-AUG-2002 (first entry)  
XX Human colon cancer related nucleotide sequence SEQ ID NO:2922.  
XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;  
XX genetic analysis; diagnostic; antisense therapy; gene; ss.  
XX Homo sapiens.  
XX WO200229086-A2.  
XX PN  
XX 11-APR-2002.  
XX PD  
XX 02-OCT-2001; 2001WO-US30732.  
XX PF  
XX 02-OCT-2000; 2000US-237271P.  
XX PR  
XX (FARB ) BAYER CORP.  
XX FA  
XX Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;  
XX Thiagalingam A, Lewis ME;  
XX WPI; 2002-426115/45.  
XX DR  
XX New isolated nucleic acid that is differentially expressed in cancer  
XX tissues useful for determining the presence of colon cancer in a cell  
XX or tissue type, and in antisense therapy .  
XX PS  
XX Claim 1; Fig 1; 796pp; English.  
XX CC ABO56306 to ABO60787 represent isolated nucleic acids (I) differentially  
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins  
XX encoded by the ABO60776 to ABO60787 nucleic acid sequences. (I) can be  
XX used in antisense therapy. An antibody immunoreactive with a polypeptide  
XX encoded by (I) is useful for detecting cancer in a patient sample, and  
XX for detecting the presence or absence of a polynucleotide encoded by a  
XX nucleic acid which hybridises to (I) in a cell. A probe/primer derived  
XX from (I) can be used for determining the presence of a nucleic acid which  
XX hybridises to (I), and for determining the phenotype of cells in a sample  
XX of cells from a patient. (I) is useful for determining the presence of  
XX colon cancer in a cell or tissue type, for determining the presence of  
XX state of other type of cancer, in antisense therapy, to generate  
XX macroarrays on a solid surface, to identify a chromosome on which the  
XX corresponding gene resides, and in tissue profiling, forensics, genetic  
XX analysis, mapping and diagnostic applications. (I) can be used to raise  
XX antibodies, and to screen for peptide analogues and antagonists.  
XX SQ Sequence 595 BP; 180 A; 124 C; 130 G; 155 T; 6 other;  
Query Match 7.2%; Score 74; DB 24; Length 595;  
Best Local Similarity 58.0%; Pred. No. 2.9e-11;  
Matches 131; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
QY 592 TTTTGGGTTCATGGCTGTTTCAAGTTTCAGTTGATTTTGGACTCTTGGCTTGGTTG 651  
DB 368 TTTTCTTGGATTCATTTGGCTTTTCCAGGCAACCTGTATGTGGACTGGTGTGATGT 309  
QY 652 TGGGCTACATCGCTTTTGACACCAAGAAATATTGAGAAGGCTCAGTTGGGTGATATGG 711  
DB 308 GTGGCTTCGCTCTTTTGTATCTCACTATTATTGAAAGGCGCAACATGAGATCAAG 249  
QY 712 ATTACGTTAAGCATGATGACCCCTTTTACAGATTTTGGCGCTGTTTGTGGCGATTTC 771  
DB 248 ATTATATCTGGCACTGCATGTATCTCTTCTTATGATTTTCTTACTGCTCTCAGAAATCA 189  
QY 772 TGATCATCATGTTTAAAGATGCAATCTGACAGGAAGAGAGAA 817

DB 188 TGATGATCTCTGCCATGATGTAAGGATAGAGAGAGAGAGAA 143  
RESULT 13  
AAV86028  
ID AAV86028 standard; cDNA; 520 BP.  
XX AC AAV86028;  
XX AC AAV86028;  
XX DT 27-APR-1999 (first entry)  
XX EST clone B115.  
XX XX  
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;  
XX tissue growth; activin; inhibitor; tumour invasion suppressor; EST; human;  
XX chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;  
XX receptor; ligand; anti-inflammatory; tumour inhibitor; ds.  
XX OS  
XX Homo sapiens.  
XX XX  
XX WO9845435-A2.  
XX PN  
XX 15-OCT-1998.  
XX PD  
XX 10-APR-1998; 98WO-US05954.  
XX PF  
XX 10-APR-1997; 97US-0835913.  
XX PR  
XX (GEMY ) GENETICS INST INC.  
XX PA  
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
XX Racie LA, Spaulding V, Treacy M;  
XX WPI; 1999-070076/06.  
XX DR  
XX New polynucleotides encoding human secreted proteins - derived from  
XX e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
XX ovary, pituitary, retina and colon cDNA libraries  
XX PT  
XX Claim 1; Page 94; 633pp; English.  
XX CC This sequence represents an expressed sequence tag (EST), and is a  
XX polynucleotide of the invention. The polynucleotides of the invention are  
XX all secreted EST sequences isolated from a variety of human tissue  
XX sources. The EST sequences and proteins encoded by them are predicted to  
XX have useful biological activities which would make them suitable for  
XX treating, preventing or ameliorating medical conditions in humans and  
XX animals, although no supporting data is given. Suggested activities  
XX include nutritional activity, immune stimulating or suppressing activity,  
XX haematopoiesis regulating activity, tissue growth activity,  
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition  
XX activity. The EST sequences are also stated to be useful for gene  
XX therapy.  
XX CC  
XX SQ Sequence 520 BP; 103 A; 140 C; 123 G; 154 T; 0 other;  
Query Match 7.0%; Score 72; DB 20; Length 520;  
Best Local Similarity 51.1%; Pred. No. 1e-10;  
Matches 227; Conservative 0; Mismatches 205; Indels 12; Gaps 2;  
QY 144 TATGATTTCTCAAAAACCTCCGCCAGATCTCCTCTCGTTCAAACTCATCTCAAGCAG 203  
DB 53 TTTGATGGCTTTTAAATTTTCTCATATAACCCCGTCACGCGAGACCTGGAAGAG 112  
QY 204 GTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTGGGGCTTACCTTCA---- 259  
DB 113 GTCTATGCAAGTTTGGCCCTTTGATGTTTGGCGGCGCTCAGGGGCTATGTCATATG 172  
QY 260 --CATCTATGGAATATCGGTGGCTCTCTCACAACATGCTTGCATGGGAGCATGGTG 317  
DB 173 GTCACTCATTTTCATTCAGGCTGGCTCTGCTGTGCTGGGCTCCCTGATTTGATGATT 232



318 TGGCTTCTCAGCTCCTTATCAAGAG-----CAAAAAGGGTGGCTCTCTGATG 371  
233 TGGCTGATGGCAACCTCATAGCCATAAAGTGAACAGAAAGACTGGGACTTCTGCT 292  
372 GCAGCTGCACATTTTGAAGGCGCTCTATTGGTCTCTGATGATGAGCTGGGCAATTAATTC 431  
293 GGATTGCACTCTTACAGGAGTTGGGCTGGGCGCTGCGCTGGAGTTTGTATGCTGTC 352  
432 GATCAGCAATGTTTGGCGCTTTTCTAGTGTCTGCTGGTGTGTTTGGTGTCTCTCA 491  
353 AACCAGCATCTTCCACATCTTTCATGGGCGGCAATGATCTTTACTGCTTACC 412  
492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGCGCTTCTTTCATCT 551  
413 CTCAGTGCACTCTATGCCAGGCGCGGCTGCTCTTCTGGGAGGTATCTTGATGTC 472  
552 GCGCTCCCTTCTCTCTGTTG 575  
473 GCGCTGAGCTTGTGCTTTGTCG 496

RESULT 14  
ABQ60318/c  
ID ABQ60318 standard; cDNA; 689 BP.

XX AC ABQ60318;  
XX DT 02-AUG-2002 (first entry)  
XX DE Human colon cancer related nucleotide sequence SEQ ID NO:4013.  
XX KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;  
XX KW genetic analysis; diagnostic; antisense therapy; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200229086-A2.  
XX PD 11-APR-2002.  
XX PF 02-OCT-2001; 2001WO-US30732.  
XX PR 02-OCT-2000; 2000US-237271P.  
XX PA (FARB ) BAYER CORP.  
XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;  
PI Thiagalingam A, Lewis ME;  
XX WPI; 2002-426115/45.

XX New isolated nucleic acid that is differentially expressed in cancer  
XX tissues useful for determining the presence of colon cancer in a cell  
XX or tissue type, and in antisense therapy -  
XX Claim 1; Fig 1; 796pp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially  
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins  
XX encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be  
XX used in antisense therapy. An antibody immunoreactive with a polypeptide  
XX encoded by (I) is useful for detecting cancer in a patient sample, and  
XX for detecting the presence or absence of a polynucleotide encoded by a  
XX nucleic acid which hybridizes to (I) in a cell. A probe/primer derived  
XX from (I) can be used for determining the presence of a nucleic acid which  
XX hybridizes to (I), and for determining the phenotype of cells in a sample  
XX of cells from a patient. (I) is useful for determining the presence of  
XX colon cancer in a cell or tissue type; for determining the presence or  
XX state of other type of cancer, in antisense therapy, to generate  
XX macroarrays on a solid surface, to identify a chromosome on which the  
XX corresponding gene resides, and in tissue profiling, forensics, genetic  
XX analysis, mapping and diagnostic applications. (I) can be used to raise

CC antibodies, and to screen for peptide analogues and antagonists.

XX Sequence 689 BP; 204 A; 157 C; 154 G; 158 T; 16 other;

XX Query Match 6.8%; Score 68.4; DB 24; Length 689;  
XX Best Local Similarity 59.3%; Pred. No. 1.3e-09;  
XX Matches 134; Conservative 0; Mismatches 91; Indels 1; Gaps 1;

QY 592 TTTTGGTGGTTCATGGCTGTTTCAAGTTTGAGTTTGATTTTGGACTCTTGGTGTG 651  
Db 349 TTTTCTTTGGATCCATTTGGCTTTTCCAGGCAACCTGATGTGGACTGGTGGT-CATG 291  
QY 652 TGGGCTACATGCTTTTGACACCCAGAAATATTGAGAGGCTCACTTGGGTGATATG 711  
Db 290 TGGGCTTGGCTTTTGGATCTCACTCATTTTGAAGGCCGCAACATGAGATCAAG 231  
QY 712 ATTACGTTAAGCATGCACTTACCCCTTTTTCACAGATTTTGGCGCTGTTTGTGCGGATTC 771  
Db 230 ATTATATCTGGCACTGCATTTGATCTCTTCTTAGATTTTCACTGCTTTCAGAAAACTCA 171  
QY 772 TGATCATCATGTTAAGAAATGCACTCTGAGAGGAGAGAGAGAGAA 817  
Db 170 TGATGATCTCGCCATGAATGAAAGGATAAGAGAGAGAGAGAGAA 125

RESULT 15  
ABQ58023/c  
ID ABQ58023 standard; cDNA; 506 BP.

XX AC ABQ58023;  
XX DT 02-AUG-2002 (first entry)  
XX DE Human colon cancer related nucleotide sequence SEQ ID NO:1718.  
XX KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;  
XX KW genetic analysis; diagnostic; antisense therapy; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200229086-A2.  
XX PD 11-APR-2002.  
XX PF 02-OCT-2001; 2001WO-US30732.  
XX PR 02-OCT-2000; 2000US-237271P.  
XX PA (FARB ) BAYER CORP.  
XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;  
PI Thiagalingam A, Lewis ME;  
XX WPI; 2002-426115/45.

XX New isolated nucleic acid that is differentially expressed in cancer  
XX tissues useful for determining the presence of colon cancer in a cell  
XX or tissue type, and in antisense therapy -  
XX Claim 1; Fig 1; 796pp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially  
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins  
XX encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be  
XX used in antisense therapy. An antibody immunoreactive with a polypeptide  
XX encoded by (I) is useful for detecting cancer in a patient sample, and  
XX for detecting the presence or absence of a polynucleotide encoded by a  
XX nucleic acid which hybridizes to (I) in a cell. A probe/primer derived  
XX from (I) can be used for determining the presence of a nucleic acid which  
XX hybridizes to (I), and for determining the phenotype of cells in a sample  
XX of cells from a patient. (I) is useful for determining the presence of  
XX colon cancer in a cell or tissue type; for determining the presence or  
XX state of other type of cancer, in antisense therapy, to generate



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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 10:14:23 ; Search time 75 Seconds  
(without alignments)  
4228.050 Million cell updates/sec

Title: US-09-955-526-3  
Perfect score: 1034  
Sequence: 1 gggcaacataacattgtct.....ataaggaaagtctctgtga 1034

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	221.2	21.4	884	4	US-09-325-932A-43
2	219.2	21.2	527	4	US-09-325-932A-44
3	122	11.8	2634	2	US-08-918-514-1
c 4	122	11.8	2634	2	US-08-918-514-2
5	122	11.8	2634	3	US-09-115-934A-1
c 6	122	11.8	2634	3	US-09-115-934A-2
7	48.8	4.7	7218	1	US-08-232-463-14
c 8	40.8	3.9	2296	2	US-08-899-336-2
9	36.8	3.6	601	4	US-09-385-982-231
10	34.6	3.3	2169	3	US-08-981-803-14
c 11	34.6	3.3	2169	3	US-08-981-803-28
12	34.6	3.3	2169	4	US-08-983-440-14
c 13	34.6	3.3	2169	4	US-08-983-440-28
14	34.6	3.3	11478	3	US-08-981-803-29
15	34.6	3.3	11478	4	US-08-983-440-29
c 16	34.4	3.3	112132	4	US-09-741-150-3
c 17	33.6	3.2	6755	3	US-08-931-999-4
18	33.4	3.2	3717	1	US-08-026-1388-7
c 19	33.2	3.2	1070	4	US-09-718-841-3
c 20	33.2	3.2	1070	4	US-09-718-810-3
c 21	33.2	3.2	1512	2	US-08-909-965C-8
c 22	33.2	3.2	1689	4	US-09-718-841-1
c 23	33.2	3.2	1689	4	US-09-718-810-1
c 24	33	3.2	688	4	US-08-998-416-915
25	32.8	3.2	2943	2	US-08-788-892-1
26	32.8	3.2	2943	2	US-09-340-475-1
27	32.4	3.1	5433	3	US-08-929-329-1

c 28	32	3.1	176373	3	US-09-128-155-17	Sequence 17, Appli
29	31.6	3.1	1418	4	US-09-111-470-7	Sequence 7, Appli
c 30	31.6	3.1	8789	1	US-08-328-254-5	Sequence 5, Appli
31	31.2	3.0	692	1	US-08-465-293A-1	Sequence 1, Appli
32	31.2	3.0	692	2	US-08-463-387A-1	Sequence 1, Appli
33	31.2	3.0	692	3	US-09-102-977-1	Sequence 1, Appli
34	31.2	3.0	692	4	US-09-034-088A-1	Sequence 1, Appli
c 35	31.2	3.0	2343	4	US-09-643-597-368	Sequence 368, App
c 36	31.2	3.0	4453	4	US-09-146-053-368	Sequence 5, Appli
c 37	31	3.0	38584	4	US-08-927-219-128	Sequence 128, App
38	31	3.0	38584	4	US-09-453-702B-50	Sequence 50, Appli
c 39	30.8	3.0	2254	4	US-09-138-277C-2	Sequence 2, Appli
40	30.8	3.0	3997	3	US-08-947-823-2	Sequence 2, Appli
41	30.8	3.0	51952	3	US-08-947-823-1	Sequence 1, Appli
42	30.6	3.0	982	3	US-08-725-532A-4	Sequence 4, Appli
c 43	30.6	3.0	1679	2	US-08-708-958-5	Sequence 5, Appli
c 44	30.6	3.0	72604	4	US-09-288-392-7	Sequence 7, Appli
c 45	30.6	3.0	72604	4	US-09-657-474-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-325-932A-43  
; Sequence 43, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; FILE OF INVENTION: death and their use in the modification of forestry plant devel  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325.932A  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 884  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-325-932A-43

Query Match	21.4%	Score	221.2;	DB	4;	Length	884;
Best Local Similarity	60.6%	Pred	No. 1.4e-52;				
Matches	383;	Conservative	0;	Mismatches	243;	Indels	6;
Gaps	1;						
Qy	203	GGGTACCTTACGCTATGCTGTCTTACTGGCATGGCTGCTGGGCTTACCTTCACAT	262				
Db	4	GGTTATTGCTGCTTAGCTGTGCCCTCGTAACAGCAGCGATCGGTGTTTATTGCACT	63				
Qy	263	TCTATGGAATATCGTGGCTCTCTACACATGCTTGCATGGGAAGCATGGTGGCT	322				
Db	64	TCTGTTGAATATGAGGGGCTCTCTACGGGCTCGCTTGCATGGTTCGTAATCGGCT	123				
Qy	323	TCTCTACGCTCTCTCTT-----ATCAAGAGCAAAAGGGTGGCTTCTTGTGAGGAGC	376				
Db	124	CTTATCGTCCCTTACTCTCTCGAACTAGGCTAAGAGCTGGCTCTCTGGCAGC	183				
Qy	377	TGCATCTTTGAAGGGCCCTCTATGCTCTCTGATGAGCTGGCATTACCTTCATCC	436				
Db	184	TGCTGCTTCAAGGGAGCTACTCTGGGACCGCTCATCGACGGGCTTATATTGATCT	243				
Qy	437	AAGCATTTGCTTTGGGGCTTTTGTAGTTGTGCTGTGGTGTGTTTGTCTCTCAGCTGC	496				
Db	244	CAGTATCTGGTGGTGGTGTGTTGTTGGACCTCTTTGGCTTGGCTTGTGTTTGGCAGC	303				
Qy	497	TGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCTTCTTTCATCTGGCT	556				
Db	304	AGCAATCACAGCCAGGAGACGGGATACCTATTTTGGAGGATATTGGGCTCGGGAAT	363				
Qy	557	CTCCCTCTCTCTGTTGGTGGCTTGTGATCTCTCATCTTTTGGTGGTTCATGCTGTTTT	616				



Db 520 GGCCTGAGCTTGTCTTTGCTCTCCCTGGGAAAT---GTTTCTTTTGGATCCATTGG 576  
2y 612 GTTTTCAAGTTTGAATCTTATTTGGACTCTTGTGTTGGGCTACATGCTCTTGAC 671  
Db 577 CTTTTCAGGAACTGTATGTGGACTGTGTGTCATGTGTGCTTGCCTTTTGTAT 636  
2y 672 ACCCAAGAAATTAATTGAGAAGGCTCACCTTGGTGATATGGAATTAAGCATGCAATG 731  
Db 637 ACTCAACTCAATTAATTGAAAGGCGCAACATGGAGATCAAGATTATATCTGGCACTGCATT 696  
2y 732 ACCCTTTTACAGATTTTGGCGCTGTTTGTGCGGATCTTGATCATCATGTTAAAGAAAT 791  
Db 697 GATCTCTTTAGATTTCAATTAATCTCTCTCAGAAAATCATGATGATCTCTGGCATGAAT 756  
2y 792 GCATCTGAGAAGGAAGAGAAGAA 817  
Db 757 GAAAGGATAAGAGAAGAGAAGAA 782

## RESULT 4

JS-08-514-2/c  
; Sequence 2, Application US/08818514  
; Patent No. 5837838  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Xu, Qunli  
; TITLE OF INVENTION: BAX Inhibitor Proteins  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Campbell & Flores  
; CITY: San Diego  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,514  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2446  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2634 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-818-514-2

Query Match 11.8%; Score 122; DB 2; Length 2634;

Best Local Similarity 51.9%; Pred. No. 1.4e-24;

Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;

QY 144 TATGATCTCTCAAAATTCGCGAGATCTCACTCTCTGTTCAAATCATCTCAAGCAG 203

Db 2535 TTTGATGCGCTTTAAATTTTCTCATATAACCCGTCACGCGACGACACCTGAAGAAG 2476

QY 204 GTGTACCTTACGCTATGCTGCTTTAGTGGCATCGGCTGGGGCTTACCTCA--- 259

Db 2475 GTCTATGGAAGTTTGGCCCTTTGTAATGTTTGGCGGCTGAGGGGCTATGTCATATG 2416

QY 260 --CAITCTATGGAATATCGGTGGCCCTCTCAAAATTAAGTGGCTTGCATGGGAAGCATGGT 317

|||||

Db 2415 GTCACTCATTTTCATTAGGCTGGCCTGCTGCTGCTTGGGCTCCCTGATATTGATGATT 2356  
QY 318 TGGCTCTCTCAGACTCCCTCTTATCAAGG-----CAAAAAGGGTGGCTCTCTCGATG 371  
Db 2355 TGGCTGATGGCAACCTCTCATAGCCATGAACGACAGAAAACCTGGACTCTTGTGT 2296  
QY 372 GCAGCTGCACCTTTTGAAGGCGCTCTATTGTCCTCTCTGATTTGAGCTGGGCATTAACCTTC 431  
Db 2295 GGAATTTGCAATTCCTTACAGGAATTTGGCCTGGGCTGCGCTGAGATTTTGTATTGCTGTC 2236  
QY 432 GATCAAGCAATGTTGTTGGCGCTTTTGTAGGTTTGTGCTGCTGCTTTTGGTGGCTTCTCA 491  
Db 2235 AACCCAGATCTCTCCACTGCTTTTCATGCGGCAAGCAATGATCTTTACCTGCTTCAAC 2176  
QY 492 GCTGCTGCATGTTTGGCAAGCGCAGAGAGTACTTGTACTCGGGGCGCTTCTTTCATCT 551  
Db 2175 CTCAGTGCACCTCTATGCCAGGCGCGTAGCTACTCTTTCTGGGAGGTATCTTGATGTCA 2116  
QY 552 GCGCTCTCCCTCTCTCTTCTGTTGCACTTTTGCATCTCCATTTTGGTGGTCCATGGCT 611  
Db 2115 GCGCTGAGCTTGTGCTTTTGTCTTCCCTGGGAAAT---GTTTCTTTGGATCCATTGG 2059  
QY 612 GTTTTCAAGTTTGAATTTGATTTTGGACTCTTGTGCTGTTGTGGGCTACATCGTCTTTGAC 671  
Db 2058 CTTTTCAGGCAACCTGTATGTGGACTGTTGGTCTCATGTGCTTCTCTCTTTTGTAT 1999  
QY 672 ACCCAAGAAATTAATTGAGAAGGCTCACTTGGTGATATGGAATTAAGCATGCAATG 731  
Db 1998 ACTCAACTCATTTATGAAAAGGCGCAACATGGAGATCAAGATTATATCTGGCACTGCATT 1939  
QY 732 ACCCTTTTACAGATTTTGGCGCTGTTTGTGGGATCTCTGATCATCATGTTTAAAGAAAT 791  
Db 1938 GATCTCTTTAGATTTTCAATTAATCTCTTTCAGAAAATCATGATGATCTCTGGCCATGAAT 1879  
QY 792 GCATCTGAGAAGGAAGAGAAGAA 817  
Db 1878 GAAAGGATAAGAGAAGAGAAGAA 1853

## RESULT 5

US-09-115-934A-1  
; Sequence 1, Application US/09115934A  
; Patent No. 6130317

; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Xu, Qunli  
; TITLE OF INVENTION: BAX Inhibitor Proteins  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/115,934A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/818,514  
; FILING DATE: 14-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 3209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001

STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
Zip: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115.934A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/818,514  
FILING DATE: 14-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 3209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2634 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-115-934A-2

Query Match 11.8%; Score 122; DB 3; Length 2634;  
Best Local Similarity 51.9%; Pred No 1.4e-24;  
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;  
Qy 144 TATGATCTCTCAAAACTTCGCGCAGATCTACCTCTCGTTCAAACTCATCTCAAGCAG 203  
Db 2535 TTGTAGTGGCTTTTAAATTTTCTCATATAACCCGCTCAACGACGACGACCTGAAGAAG 2476  
Qy 204 GTGTACCTACGATATGCTGCTTTAGTGGCATCGGCTGCTGGGGCTTACCTCA 259  
Db 2475 GTCTATGCAAGTTTGGCTTTGATGTTGTTGGGGCTGTCAGGGGCTATGTCATATG 2416  
Qy 260 --CATTTCTATGGAATATCGTGGCTCTCTCAACAATGCTTGCATGGGAAGATGGT 317  
Db 2415 GTCACTCATTTCACTTACGCTGGCTGCTGCTGCTGGGCTCCCTCATATGATGATT 2356  
Qy 318 TGGCTTCTCTCAGCTCTCTTATCAAGAG-----CAAAAAGGGTGGCTTCTTGATG 371  
Db 2355 TGGCTGATGGCAACCTCATAGCCATGAACCTGAACAGAAAAAACTGGGACTTCTTCT 2296  
Qy 372 GCAGCTGCATTTTGAAGGCGCTCTATTTGCTCTCTGATTTGAGCTGGGCATTAATTC 431  
Db 2295 GGATTTGCAATTCCTTACAGAAATGGCTGGGCTGGGCTGGCTGCTGCTGCTGCTGCT 2236  
Qy 432 GATCCAGCATTTGTTGGCGCTTTGAGGTTGCTGTTGCTGTTGTTGTTGTTGTTGTTGCTCA 491  
Db 2235 AACCCAGCATCTCTCCCATCTGTTTTCATGGGCAAGCAATGATCTTACCTGCTTCAAC 2176  
Qy 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGCTTCTTTCATCT 551  
Db 2175 CTCAGTGCATCTATGCCAGGCGCGTAGCTACCTCTTCTGGAGGTATCTTGTATGTCAT 2116  
Qy 552 GGGCTCTCCCTCTCTTCTGTTGTCATTTGTCATCTCTCAATTTTGGTGGTTCCATGCT 611  
Db 2115 GCGCTGAGCTTGTGTTTGTCTTCCCTGGGGAAT---GTTTTCTTTGGATCCATTTGG 2059  
Qy 612 GTTTTCAAGTTTGAAGTTGATTTTGGACTCTTGGTGTGTTTGGGGCTACATCGTCTTTCAC 671  
Db 2058 CTTTTCCAGCAACCTGTATGTTGGGACTGTTGGTGCATGTTGGCTTCTGCTCTCTTTGAT 1999  
Qy 672 ACCCAAGAAATATTAGAGAGGCTCACTTGGGTGATATGATTAAGCATGCAATG 731

TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2634 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-115-934A-1  
Query Match 11.8%; Score 122; DB 3; Length 2634;  
Best Local Similarity 51.9%; Pred No 1.4e-24;  
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;  
Qy 144 TATGATCTCTCAAAACTTCGCGCAGATCTACCTCTCGTTCAAACTCATCTCAAGCAG 203  
Db 100 TTGTAGTGGCTTTTAAATTTTCTCATATAACCCGCTCAACGACGACGACCTGAAGAAG 159  
Qy 204 GTGTACCTACGATATGCTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCA----259  
Db 160 GTCTATGCAAGTTTGGCCCTTTGATGTTTGTGGGCTGTCAGGGGCTTATGTCATATG 219  
Qy 260 --CATTTCTATGGAATATCGTGGGCTCTCTCAACAATGCTTGCATGGGAAGCATGGT 317  
Db 220 GTCACTCATTTCACTAGGCTGGCTCTGCTGCTGCTGGCTCCCTGATATTTGATGATT 279  
Qy 318 TGGCTTCTCAGCTCTCTCTTATCAAG-----CAAAAAGGGTGGCTTCTTGATG 371  
Db 280 TGGCTGATGGCAACCTCTATGACCATGAACCTGAACAGAAAAAACTGGGACTTCTTGTCT 339  
Qy 372 GCAGCTGCATCTTTTGAAGGCGCTCTATTTGCTCTCTGATTCAGCTGGGCTTAACTTC 431  
Db 340 GGAATTTGCAATTCCTTACAGAAATGGCTGGGCTGGCTGGGCTTGTATGCTGTC 399  
Qy 432 GATCAAGCATGTTTGGGCTTTTGTAGTGTGCTGCTGCTGCTTTTGGTGGCTTCTCA 491  
Db 400 AACCCAGCATCTTCCCATCTGCTTTTCATGGGCAAGCAATGATCTTACCTGCTTCAAC 459  
Qy 492 GCTGCTGCATGTTTGAAGGCGCAGGAGTACTTGTACCTCGGGGCTTCTTTCATCT 551  
Db 460 CTCAGTGCATCTATGCGAGGCGCTGAGTACCTCTTCTGGAGGTATCTTGATGICA 519  
Qy 552 GGGCTCTCCCTTCTCTGCTGCTGCTTGTGATCTTGCATCTTCCATTTTGGTGGTTCATGGCT 611  
Db 520 GCGCTGAGCTTGTGCTTTGCTCTTCCCTGGGAAAT---GTTTTCTTTGGATCCATTTGG 576  
Qy 612 GTTTTCAAGTTTGAAGTTGATTTTGGACTCTTGGTGTGTTGTTGGCTACATCGTCTTTGAC 671  
Db 577 CTTTTCAGGCAACCTGTATGCGGACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636  
Qy 672 ACCCAAGAAATATTGAGAGGCTCTCTTGGGTGATATGATTAAGTTAAGCATGATG 731  
Db 637 ACTCAACTCATTTTGAAGGCGCGAATGAGATCAAGATTAATATCTGGCACTGCATT 696  
Qy 732 ACCCTTTTCAGATTTTGGGCTGTTTGTGGGATTTCTGATCATCATGTTTAAAGAAAT 791  
Db 697 GATCTTCTTGAATTTCACTTCTTCTTCAAAAACCTCATGATGATCTTGGCCATGAAT 756  
Qy 792 GCATCTGAGAGGAAGAGAGAGAA 817  
Db 757 GAAAAGGATAAGAGAGAGAGAGAA 782

RESULT 6  
US-09-115-934A-2/c  
Sequence 2, Application US/09115934A  
Patent No. 6130317  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Xu, Qunli  
TITLE OF INVENTION: BAX Inhibitor Proteins  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP

Db 1998 ACTCAACTATTGAAAGCCGACATGAGATCAAGATTATATCTGCGACTGCATT 1939  
QY 732 ACCCTTTTACAGATTTGGCGCTGTTTGTGCGATTCTGATCATCATGTTAAAGAAT 791  
Db 1938 GATCTCTTCTAGATTCTACTGCTTTCAGAAAACATCATGATCCTGGCCATGAAT 1879  
QY 792 GCATCTGAGAGAGAGAGAGAA 817  
Db 1878 GAAAGGATAAGAGAGAGAGAA 1853  
RESULT 7  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZ95F-Fls  
US-08-232-463-14  
Query Match 4.7%; Score 48.8; DB 1; Length 7218;  
Best Local Similarity 3.6%; Pred. No. 0.00065;  
Matches 14; Conservative 217; Mismatches 159; Indels 0; Gaps 0;  
QY 297 GCTTGGATGGGAACATGGTGGCTTCTCTCAGCTCCCTCATCAAGAGCAAAAAGG 356  
Db 1058 GCTTGGATGGATTT 1117  
QY 357 GTGGCTCTCTGATGGAGCTGACCTTTTTTGAAGGCGCTCTATTGCTCTGATGAG 416  
Db 1118 YY 1177

QY 417 CTGGCATTAACTTCGATCCCAAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTT 476  
Db 1178 YY 1237  
QY 477 TTTGTTGCTTCTCAGCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACCTCGG 536  
Db 1238 YY 1297  
QY 537 GGCCTTCTTTCATCTGGCGTCTCCCTCTCTCTCTGTTGACATTCCTCCATTTT 596  
Db 1298 YY 1357  
QY 597 GGTGTTCCATGGCTGTTTCAAGTTTGAGTTGATTTGAGCTCTTGTGTTGTTGGC 656  
Db 1358 YY 1417  
QY 657 TACATCGCTTTGACACCCAGAAATTT 686  
Db 1418 YYYYYYYYYYYYYYYYGTACCAATTTCTT 1447  
RESULT 8  
US-08-899-336-2/c  
; Sequence 2, Application US/08899336  
; Patent No. 5955649  
; GENERAL INFORMATION:  
; APPLICANT: HIROTA, NAOHICO  
; APPLICANT: KIHARA, MAKOTO  
; APPLICANT: KURODA, HISAO  
; APPLICANT: ITO, KAZUTOSHI  
; TITLE OF INVENTION: GENE EXPRESSION REGULATORY DNA,  
; TITLE OF INVENTION: EXPRESSION CASSETTE, EXPRESSION VECTOR AND TRANSGENIC  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,336  
; FILING DATE: 23-JUL-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP HEI 8-193433  
; FILING DATE: 23-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORVAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 2589-0061-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2296 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-899-336-2  
Query Match 3.9%; Score 40.8; DB 2; Length 2296;  
Best Local Similarity 52.3%; Pred. No. 0.07;  
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;





Db 1743 GAGTTTATGATTAAGTTCATCTTATGATATGATTAACATCTTATTATAGATGCATATA 1684  
Qy 810 AAGAAGAAGAAGAGGAGAACTAGATTG 838  
Db 1683 AATAGCTAATGATAGAACATTGACATTG 1655

RESULT 12  
US-08-983-440-14  
; Sequence 28, Application US/08983440  
; Patent No. 6232122  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, Peter  
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION  
; FILE REFERENCE: 674509-2003  
; CURRENT APPLICATION NUMBER: US/08/983,440  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 9514437.4  
; EARLIER FILING DATE: 1995-07-14  
; EARLIER APPLICATION NUMBER: PCT/EP96/03053  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
US-08-983-440-14

Query Match 3.3%; Score 34.6; DB 4; Length 2169;  
Best Local Similarity 47.8%; Pred. No. 3.7;  
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 630 TATTTGGACTCTTGCTGTTGCTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689  
Db 307 TATTTGTTCTCTTATTATTATATATATATATATATATATATATATATATATATAT 366

Qy 690 AAGGCTCATTGGTGATATGATTAAGCTTAAGCATGATGACCTTTTTCACAGATTTT 749  
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426

Qy 750 GCGCTGTTTTGTCGGATTCATCATCTTAAAGATGATCTGAGAGGAGAG 809  
Db 427 GAGTTTATGATTAAGTTCATCTTAGAATATGAATTTAACTATTATATAGATGCATATA 486

Qy 810 AAGAAGAAGAAGAGGAGAACTAGATTG 838  
Db 487 AATAGCTAATGATAGAACATTGACATTG 515

RESULT 13  
US-08-983-440-28/c  
; Sequence 28, Application US/08983440  
; Patent No. 6232122  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, Peter  
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION  
; FILE REFERENCE: 674509-2003  
; CURRENT APPLICATION NUMBER: US/08/983,440  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 9514437.4  
; EARLIER FILING DATE: 1995-07-14  
; EARLIER APPLICATION NUMBER: PCT/EP96/03053  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
US-08-983-440-28

Query Match 3.3%; Score 34.6; DB 4; Length 2169;  
Best Local Similarity 47.8%; Pred. No. 3.7;  
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 630 TATTTGGACTCTTGCTGTTGCTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689  
Db 307 TATTTGTTCTCTTATTATTATATATATATATATATATATATATATATATATATAT 366

Qy 690 AAGGCTCATTGGTGATATGATTAAGCTTAAGCATGATGACCTTTTTCACAGATTTT 749  
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426

Qy 750 GCGCTGTTTTGTCGGATTCATCATCTTAAAGATGATCTGAGAGGAGAG 809  
Db 427 GAGTTTATGATTAAGTTCATCTTAGAATATGAATTTAACTATTATATAGATGCATATA 486

Qy 810 AAGAAGAAGAAGAGGAGAACTAGATTG 838  
Db 487 AATAGCTAATGATAGAACATTGACATTG 515

RESULT 14  
US-08-981-803-29  
; Sequence 29, Application US/08981803  
; Patent No. 6147279  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, PETER  
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION  
; FILE REFERENCE: 674509-2004  
; CURRENT APPLICATION NUMBER: US/08/981,803  
; CURRENT FILING DATE: 1997-04-17  
; EARLIER APPLICATION NUMBER: PCT/EP96/03052  
; EARLIER FILING DATE: 1996-07-12  
; EARLIER APPLICATION NUMBER: 9514435.8  
; EARLIER FILING DATE: 1995-07-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11478  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
US-08-981-803-29

Query Match 3.3%; Score 34.6; DB 3; Length 11478;  
Best Local Similarity 47.8%; Pred. No. 7.5; 109; Indels 0; Gaps 0;

Qy 630 TATTTGGACTCTTGCTGTTGCTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689  
Db 307 TATTTGTTCTCTTATTATTATATATATATATATATATATATATATATATATATAT 366

Qy 690 AAGGCTCATTGGTGATATGATTAAGCTTAAGCATGATGACCTTTTTCACAGATTTT 749  
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426

Qy 750 GCGCTGTTTTGTCGGATTCATCATCTTAAAGATGATCTGAGAGGAGAG 809  
Db 427 GAGTTTATGATTAAGTTCATCTTAGAATATGAATTTAACTATTATATAGATGCATATA 486

Qy 810 AAGAAGAAGAAGAGGAGAACTAGATTG 838  
Db 487 AATAGCTAATGATAGAACATTGACATTG 515

RESULT 15  
US-08-983-440-29  
; Sequence 29, Application US/08983440  
; Patent No. 6232122  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, Peter  
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION  
; FILE REFERENCE: 674509-2003  
; CURRENT APPLICATION NUMBER: US/08/983,440

; CURRENT FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 9514437.4  
; EARLIER FILING DATE: 1995-07-14  
; EARLIER APPLICATION NUMBER: PCT/EP96/03053  
; EARLIER FILING DATE: 1996-07-12  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11478  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(11478)  
; OTHER INFORMATION: B stands for G or C or T/U  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(11478)  
; OTHER INFORMATION: R stands for G or A  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(11478)  
; OTHER INFORMATION: K stands for G or T/U  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(11478)  
; OTHER INFORMATION: W stands for A or T/U  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(11478)  
; OTHER INFORMATION: M stands for A or C  
; US-08-993-440-29

Query Match 3.3%; Score 34.6; DB 4; Length 11478;  
Best Local Similarity 47.8%; Pred. No. 7.5;  
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;  
Qy 630 TATTTGGACTCTTGGTGTGTTGGGTACATCGTCTTGACACCCAGAAATTTAG 689  
Db 307 TATTTGTCTCTTATTATTATTATCATACATATTATTACAGGAAGACAGTACA 366  
Qy 690 AAGGCTCACTTGGGTGATATGGATTAGCTTAAGCATGCAATGACCCCTTTTCACAGATTTT 749  
Db 367 CAGATCTTAACGTTTATGTTCAATCAACTTTTGGAGCATTTGACAGTACCACAAATTTT 426  
Qy 750 GCGGCTGTTTTTGTCCGATCTCATCATGTTAAAGATGCACTGAGAGGAGAG 809  
Db 427 GAGTTTATGATTAAGTTCAATCTTTAGAAATATGAATTTTACATCTATTATAGATGCATAA 486  
Qy 810 AAGAGAAGAGAGAGAGAACTAGATTG 838  
Db 487 ATAGCTAATGATAGACATTCACATTG 515

Search completed: May 25, 2003, 11:26:51  
Job time : 90 secs

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 11:00:18 ; Search time 165 Seconds  
(without alignments)  
8274.897 Million cell updates/sec

Title: US-09-955-526-3  
Perfect score: 1034  
Sequence: 1 gagcaacatacaattgtct.....ataaggaagtctctgtga 1034

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues  
Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
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2: /cgn2\_6/prodata/2/pubna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/prodata/2/pubna/US05\_NEW\_PUB.seq:  
4: /cgn2\_6/prodata/2/pubna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/prodata/2/pubna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/prodata/2/pubna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/prodata/2/pubna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/prodata/2/pubna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/prodata/2/pubna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/prodata/2/pubna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/prodata/2/pubna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/prodata/2/pubna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/prodata/2/pubna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/prodata/2/pubna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	1033.	99.9	1034	9	US-09-955-526-3
2	429.	41.5	1735	9	US-10-167-015-15
3	428.8	41.5	1009	10	US-09-770-445-223
4	417.4	40.4	989	9	US-10-167-015-17
5	411	39.7	1218	9	US-10-219-220-232
6	314.4	30.4	1026	9	US-10-167-015-31
7	312	30.2	957	9	US-10-167-015-1
8	310.4	30.0	1138	9	US-10-167-015-33
9	310.4	30.0	1139	9	US-10-167-015-5
10	305	29.5	1026	9	US-10-167-015-3
11	245.6	23.8	1102	9	US-10-219-220-231
12	221.2	21.4	884	9	US-10-219-220-43
13	219.2	21.2	527	9	US-10-219-220-44
14	178.8	17.3	740	9	US-10-167-015-7
15	172.8	17.2	308	9	US-10-167-015-22
16	172.8	16.7	376	10	US-09-878-574-1827
17	157.8	15.3	234	9	US-10-167-015-19
18	125.2	12.1	2922	10	US-09-923-302-73
19	125.2	12.1	2994	12	US-10-044-090-356

ALIGNMENTS

RESULT 1

US-09-955-526-3  
; Sequence 3, Application US/09955526  
; Publication No. US20030009785A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods  
; FILE REFERENCE: P-LJ 4868  
; CURRENT APPLICATION NUMBER: US/09/955,526  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/661,014  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1034  
; TYPE: DNA  
; ORGANISM: Lycopodium esculentum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (87)...(830)  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1034)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-955-526-3

Query Match 99.9%; Score 1033; DB 9; Length 1034;  
Best Local Similarity 100.0%; Pred. No. 3.2e-313;  
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAACATACATTGTCTACGTTTCAGATAATATCTTGTCTCATTTCAGTTCACAAA 60  
Db 1 GAGCAACATACATTGTCTACGTTTCAGATAATATCTTGTCTCATTTCAGTTCACAAA 60  
QY 61 ACTCGAAG 120  
Db 61 ACTCGAAG 120  
QY 121 CTGCTCTCGACCCGCTGAGTTATGATTCTCAAAAACCTTCGCGAGATCTCACCTC 180  
Db 121 CTGCTCTCGACCCGCTGAGTTATGATTCTCAAAAACCTTCGCGAGATCTCACCTC 180



## RESULT 3

US-09-770-445-223  
; Sequence 223, Application US/09770445

; Patent No. US20020023281A1

; GENERAL INFORMATION:

; APPLICANT: Goriach, Jörn

; APPLICANT: An, Jong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kriker, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurlban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 223

; LENGTH: 1009

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-770-445-223

Query Match 41.5%; Score 428.8; DB 10; Length 1009;

Best Local Similarity 73.7%; Pred. No. 1e-123;

Matches 560; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 72 AAGAAGAGACATGAGAGTTTCACATGCTTTTCGACTCGCATCTGCTCTGCG 131

DB 23 AAAAAAAGCAAAATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 79

QY 132 AACCGCTGGAGTTATGATTTCTCAAAAATTCGCGCAGATCTCACCTCTCGTTCAAACT 191

DB 80 AGAAGCTGGAGCTATGATTTCTTAAAACTTCGTCAGATTTCTCCAGCGTTCAAGAT 139

QY 192 CATCTCAAGCAGGTGTACCTTACCTATGCTGTGCTTTAGTGGCATCGGCTCGGGCT 251

DB 140 CATCTTAAACGGGTATTTGACCTTATGTTGCTCTCTCTCTCTCTCTCTCTCTCTCT 199

QY 252 TACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGCTTGATGGGAAGC 311

DB 200 TACCTTCATGCTCTGGAATATCGCGGTATTTCTTAAACGATTTGATTTGGAAT 259

QY 312 ATGCTGTGGCTTTCTCAGCTCTCTCTTATCAAGACAAAAAGGTGGCTCTCTGATG 371

DB 260 ATGATTTGGCTCTCTTATGCTCTCTTATGAACACCAAAAAAGGTCTCTCTCTCTCT 319

QY 372 GCAGCTGCACTTTTGAAGCGCTCTATTTGGTCTCTGATTTGAGCTGGGCAATTAATTC 431

DB 320 GCGTCTGCTGTTCTGGAAGGTGCTCTGTTGGCCCTTATCAAGTGGCAATGATGTT 379

QY 432 GATCCAGCATTTGTTTGGCGCTTTTGTAGGTGTGCTGTGTTTGGTCTCTCTCA 491

DB 380 GACCAAGCATTCCTATCACTGCGTTTGTGGAACGCGATAGCGTTTCTGTCTCTCA 439

QY 492 GCTGCTGCCATGTTGGCAAGCGGAGGAGTACTGTACTCTCGGGGCGCTCTCTTCACT 551

DB 440 GCAGCAGCAATGTTAGCAAGCAGCGAGGATATCTTACCTTGGAGACTGCTTTTCACT 499

QY 552 GCGCTCTCCCTTCTCTTCTGTTGCACTTTGCACTCTTCCATTTTGGTGTGTTCCATGGCT 611

DB 500 GCGTGTCTATGCTAAATGTGCTCCAGTTTGCCTCTCTCGATCTTTGGTGGCTCTGCACT 559

QY 612 GTTTTCAAGTTTGAAGTTTGGGACTCTTGGTGTGTTTGGGCTACATCGTCTTTGAC 671

DB 560 ATCTTTAAGTTTGAAGTTTGTATCTTTGGACTTTTGAATCTTTTGGATACATGTTGGTGGAC 619

QY 672 ACCCAAGAAATTTATGAGAAGGCTCACTTGGGTGATATGGAATACGTTAAGCATGCAATTG 731

DB 620 ACACAAGAGATTATAGAAAAGGCACACCTCGGTGACATGATGTAAACCATTCGTTG 679

QY 732 ACCCTTTTACAGATTTTGGCGCTGTTTGTGGGATTTCTGATCATCATGTTTAAAGAAAT 791

DB 680 ACCCTTTTACATGACTTTTGTAGCTGTGTTTGTTCGGAATTTCAATATAATGTTGAAGAAC 739

QY 792 GCATCTGAGAAGGAAGAGAGAAGAAGAAGAGAGAGAACT 831

DB 740 TCAGCAGATATAAGAGAGAGAAGAAGAAGAAAGAGAGAACT 779

## RESULT 4

US-10-167-015-17

; Sequence 17, Application US/10167015

; Publication No. US20030056249A1

; GENERAL INFORMATION:

; APPLICANT: Simmons, Carl R.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Jonaal, Gurmukh

; APPLICANT: Acevedo, Pedro A. Navarro

; APPLICANT: Tao, Yumin

; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use

; FILE REFERENCE: Thereof

; CURRENT APPLICATION NUMBER: US/10/167,015

; CURRENT FILING DATE: 2002-06-11

; PRIOR APPLICATION NUMBER: US 60/297,478

; PRIOR FILING DATE: 2001-06-12

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 989

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (37)...(822)

US-10-167-015-17

Query Match

Best Local Similarity 40.4%; Score 417.4; DB 9; Length 989;

Matches 526; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 120 TCTGCTCTCGCAACCGCTGCGAGTTATGATTTCTCAAAAACTTCCGCGAGATCTCACCT 179

DB 67 TCTTCTTCGAGAAGCGCTGGAGTTACGATAGTCTCAAGAAATTTCCGTGAGATCTCTCG 126

QY 180 CTGTTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCG 239

DB 127 CTGGTTTCAAGATCATCAAAACGGGTTTATTTTACGTTATGTTGGCTGTGGTGGCTGT 186

QY 240 GCTGCTGGGCGCTTACCTTCACATTTCTATGGAATATCGGTGGCCCTTCCACAACTAGT 299

DB 187 GCTGTTGGAGCTTTCTTCACTGTTCTGTTGAACATGTTGGGTTTCTCACACCTTGGCT 246

QY 300 TGATGGGAAGCATGTTGGGCTTCTCTCAGTCTCTCTTATCAAGACCAAAAGGGTG 359

DB 247 TCCATTTGAAGCATGTTGGTTGCTATCTACCCCTTGTGAAGAGCAAAAGAGGTTG 306

QY 360 GCTCTTCTGATGCGAGTGCATCTTTTGAAGCGGCTCTATTGGTCTCTGATTTGAGCTG 419







```
;
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(912)
US-10-167-015-33

Query Match      30.0%; Score 310.4; DB 9; Length 1139;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 96 TTCAATGTTTTCGACTCGCAATCTGCTCTCGCAACCGCTGGAGTTATGATTTCTCTC 155
Db 166 TCCTCCACGTCGTGCGCGCGTACGCGCGCGCGGAGGCTGGGCTACGACTCGATG 225
Qy 156 AAAAATTCGCGCAGATCTCACCTCTCTGTTCAAATCATCTCAAGCAGGTGTACTTACG 215
Db 226 AAGAACTTCGCGCAGATCAGCCCGCGCTCCAGACCCACCTCAAGCTCGTTTACCTCACC 285
Qy 216 CTATGCTGTCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCATGGAATATC 275
Db 286 CTATGCTGGCGCTGCGCTCTGTCGCGGCTGGGCGGTACCTGCACGTCGTGGAACATC 345
Qy 276 GGTGGCTCTCTCAACAATGCTTTCATGGAAGAGATGGTGTGCTTCTCTCAGCTCT 335
Db 346 GCGGAGATGTGACCATGCTCGGCTGCTCGGAGCATGCGCTCTCTCTCGGTGCC 405
Qy 336 CCTTATCAAGAGCAAAAAGGTTGCTTTTGGTGTCTCTCAGTGGCAAGCTTTTGAAGCGCC 395
Db 406 GTCTACGAGAGAGAGAGGTTACTGGCTGCTGATGGCGGCTGCCCTCTCTGGAAGGCG 465
Qy 396 TCATATGGTCTCTGATGAGCTGGGCAATACTTCGATCCAAAGCATTTGTTGGCGCT 455
Db 466 TCGTTGAGACCCCTCATCAAGCTCGCGCTGGAATTGACCCAGCATCTCTGTGACAGCG 525
Qy 456 TTTGTAGGTTGTCTGTGGTTTTTGGTTGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGC 515
Db 526 TCTGTGGGACTGCGCATGCGTTGCGTGCTGCTGATGGCGGCTGCCCTCTCTGGAAGGCG 585
Qy 516 AGGAGTACTTGTACCTCGGGGCTTCTTTTTCATCTGGGCTCTCTCTCTCTCTCTCTCT 575
Db 586 AGGAGTACTTGTACCTCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 645
Qy 576 CACTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 632
Db 646 CAGTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 705
Qy 633 TTTGAGCTCTTGTGTTTGTGGCTACATCGTCTTTGACCCCAAGAAATTTAGAGAG 692
Db 706 TTTGGGCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 765
Qy 693 GCTCATTGGGTGATGATGATTACGTTAAGCATGATTCACCTTTTTCACAGATTTTGGC 752
Db 766 GCGCACCACGCGCATGACTACATCAGCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 825
Qy 753 GCTGTTTGTGCGGATTCATCATGTTTAAAGATTCATGAGTGTGAGAGGAGAGAG 812
Db 826 GCTGTCTTGTCTCGCATCTTGTCTATCATGCTCAAGACGCGCTGCAAGTCTGAGGAC 885
Qy 813 AAGAGAGAGAGAGAA 828
Db 886 AAGAGAGAGAGAGAA 901

;
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(993)
US-10-167-015-5

Query Match      30.0%; Score 310.4; DB 9; Length 1139;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 96 TTCAATGTTTTCGACTCGCAATCTGCTCTCGCAACCGCTGGAGTTATGATTTCTCTC 155
Db 166 TCCTCCACGTCGTGCGCGCGTACGCGCGCGCGGAGGCTGGGCTACGACTCGATG 225
Qy 156 AAAAATTCGCGCAGATCTCACCTCTCTGTTCAAATCATCTCAAGCAGGTGTACTTACG 215
Db 226 AAGAACTTCGCGCAGATCAGCCCGCGCTCCAGACCCACCTCAAGCTCGTTTACCTCACC 285
Qy 216 CTATGCTGTCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCATGGAATATC 275
Db 286 CTATGCTGGCGCTGCGCTCTGTCGCGGCTGGGCGGTACCTGCACGTCGTGGAACATC 345
Qy 276 GGTGGCTCTCTCAACAATGCTTTCATGGAAGAGATGGTGTGCTTCTCTCAGCTCT 335
Db 346 GCGGAGATGTGACCATGCTCGGCTGCTCGGAGCATGCGCTCTCTCTCGGTGCC 405
Qy 336 CCTTATCAAGAGCAAAAAGGTTGCTTTTGGTGTCTCTCAGTGGCAAGCTTTTGAAGCGCC 395
Db 406 GTCTACGAGAGAGAGAGGTTACTGGCTGCTGATGGCGGCTGCCCTCTCTGGAAGGCG 465
Qy 396 TCATATGGTCTCTGATGAGCTGGGCAATACTTCGATCCAAAGCATTTGTTGGCGCT 455
Db 466 TCGTTGAGACCCCTCATCAAGCTCGCGCTGGAATTGACCCAGCATCTCTGTGACAGCG 525
Qy 456 TTTGTAGGTTGTCTGTGGTTTTTGGTGTCTCTCAGTGGCAAGCTTTTGAAGCGCGC 515
Db 526 TTTGTGGGACTGCGCATGCGTTGCGTGCTTCTCTGCGCGCATGTTGGCCAAAGCGC 585
Qy 516 AGGAGTACTTGTACCTCGGGGCTTCTTTTTCATCTGGGCTCTCTCTCTCTCTCTCTCT 575
Db 586 AGGAGTACTTGTACCTCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 645
Qy 576 CACTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 632
Db 646 CAGTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 705
Qy 633 TTTGAGCTCTTGTGTTTGTGGCTACATCGTCTTTGACCCCAAGAAATTTAGAGAG 692
Db 706 TTTGGGCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 765
Qy 693 GCTCATTGGGTGATGATGATTACGTTAAGCATGATTCACCTTTTTCACAGATTTTGGC 752
Db 766 GCGCACCACGCGCATGACTACATCAGCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 825
Qy 753 GCTGTTTGTGCGGATTCATCATGTTTAAAGATTCATGAGTGTGAGAGGAGAGAG 812
Db 826 GCTGTCTTGTCTCGCATCTTGTCTATCATGCTCAAGACGCGCTGCAAGTCTGAGGAC 885
Qy 813 AAGAGAGAGAGAGAA 828
Db 886 AAGAGAGAGAGAGAA 901

;
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; Sequence 5, Application US/10/167,015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A.
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
```



Db 694 CACACAGATGATCATCGAGAAAGCGACCAATGAGACTATGATTAATTTAAACATTCAC 753  
Qy 731 GACCCCTTTACAGATTTGGCGCTGTTTTGTGCGGATTTCTGATCATCATGTTAAAGAA 790  
Db 754 GGACCTCTTACATTCGTTGCTGTATTGTTGCTGATGCTCATATGCGCAAGAA 813  
Qy 791 TGCATCTGAGNAGAGAGAGAGAGAGAGAGAGAGAA 828  
Db 814 TGCAGACAGTAATCCAGGAGGAGGAGGAGGAGAGAA 851

RESULT 12  
US-10-219-220-43  
; Sequence 43, Application US/10219220  
; Publication No. US2003008274A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of plant development  
; FILE REFERENCE: 11000.1022c1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 884  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-219-220-43

Query Match 21.4%; Score 221.2; DB 9; Length 884;  
Best Local Similarity 60.6%; Pred. No. 1.2e-58;  
Matches 383; Conservative 0; Mismatches 243; Indels 6; Gaps 1;

Qy 203 GGTGTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGCTGGGCTTACCTTACAT 262  
Db 4 GGTTTATTTGTCGTAGCTGTGCTGCTGTAACAGACGATCGGTGTTTATTTGCTATCT 63

Qy 263 TCTATGGAATATCGGTGCTCTCTCACAAATGGCTTGTATGGAGAGATGCTGTGGCT 322  
Db 64 TCTGTGATATGAGGGCTCTCTACGGGCTCGCTTGCATTGTTCTGTAATCGGCT 123

Qy 323 TCTCTAGCT 376  
Db 124 CTATCCCT 183

Qy 377 TGCACCTTTTGAAGCGCTCTATTTGTCCTCTGATTGAGCTGGGCAATTAACCTCGATCC 436  
Db 184 TGTGCTGTTCAAGGAGTACTCTGGGACCGCTCATCGCGGTCAATTAATGACTC 243

Qy 437 AAGCATTTGTTTGGCGCTTTTGTAGTTGTGCTGTTGTTTGTGCTTCTCAGCTGC 496  
Db 244 CAGTATCTGTTGAGTGGCTTTGTTGGACCTCTTTGGCTCTGCTTTGCTTTTTCGGCAGC 303

Qy 497 TGCATGTTGGCAAGCGCAGGAGTACTTGTACTCGGGGCTCTCTCTCTCTCTCTCTCTCT 556  
Db 304 AGCAATCAGCAGGAGAGCGGGAATACCTATTTTGGAGATATTTGGCTCGGAAT 363

Qy 557 CTCCCT 616  
Db 364 CAGCATATTTGATGCTGCAACTAGCATCTCTGATTTTGTGCTGTTCTCTGCGGATTA 423

Qy 617 CAGTTTGTAGTTGATTTTGGACTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 676  
Db 424 CAGTTTGTAGTTGATTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483

Qy 677 AGAATATTGAGAGGCTCTCTCTGTTGATGATGATGATGATGATGATGATGATGATGATG 736  
Db 484 GATGATCATCGAGAAAGCGGACCATGAGACTATGATTTATTTAAACATTCACCTGGACCT 543

Qy 737 TTTCACAGATTTGGCGCTGTTTTGTGCGGATTTCTGATCATCATGTTAAGATGCTATC 796  
Db 544 CTTCAATTGACTTCGTTGCTGTATTGTTGCTGATGCTATAATGCGCAAGATGCGAGA 603

Qy 797 TGAGAAGGAGAGAGAGAGAGAGAGAGAGAGAA 828  
Db 604 CAGTAATCCAGGAGGAGGAGGAGGAGAGAA 635

RESULT 13  
US-10-219-220-44  
; Sequence 44, Application US/10219220  
; Publication No. US2003008274A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of plant development  
; FILE REFERENCE: 11000.1022c1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 527  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-219-220-44

Query Match 21.2%; Score 219.2; DB 9; Length 527;  
Best Local Similarity 74.5%; Pred. No. 3.6e-58;  
Matches 289; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

Qy 130 GCACCCCTCGAGTTATGATTTCTCTCAAAAATTTCCGCCAGATCTCACCTCTCGTTCAA 189  
Db 141 GCAAGGGGTGAGCCCGATTCCTCAAGAACTTCGCCAGATACTCCGCCGTCCAAT 200

Qy 190 CTATCTCAAGAGGTGTACCTTACCTATGCTGTGCTTGTAGTGCATCGGTGCTGGG 249  
Db 201 CTCACCTCAAGAAATGTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 260

Qy 250 CTTACCTTCATCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTCATCGGAA 309  
Db 261 CTTACCTTCATCTATGCTGAACATCGGGGCTCTCTCAACAATGGCTTCATCGGAA 320

Qy 310 GCATGTTGGCTTCTCTAGCT 369  
Db 321 GCATCGTGGCT 380

Qy 370 TGGCAGCTGCACCTTTTGAAGGCGCTCTATTTGCTCTCTGATTGAGCTGGCAATTA 429  
Db 381 TGGGCGGCTCTCTTTGAAGGAGCGTATCGTCTCTCTCAAGCGGCAATTAAGG 440

Qy 430 TCGATCAAGCATTTGTTGGCGCTTTTGTAGGTTGCTGTTGTTGTTGTTGTTGTTGTTG 489  
Db 441 TCGACCCGAGCATTTGATTAAGCGCATTTTGGGATCTCGCTGGCTTCGCTTGTCTTCT 500

Qy 490 CAGCTGCTGCCATCTTGGCAAGCGGAG 517  
Db 501 CGGCGGAG-CATGTTGGCTAGCGGAG 527

RESULT 14  
US-10-167-015-7  
; Sequence 7, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Johal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro

```

; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 740
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(489)
US-10-167-015-7

Query Match      17.3%; Score 178.8; DB 9; Length 740;
Best Local Similarity 64.0%; Pred No. 2.1e-45;
Matches 270; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 404 TCCTCTGATGAGCTGGGCAATTAACCTGATCCAGACATGCTGTTGGCGCTTTGAGG 463
DB 57 TGCTTAGATGACGAATGGCTGTTTTCCTCCATCATCTGTCGACGGGCTTCGTGGG 116
QY 464 TTGTGCTGTGTTTTGTTGTTCTCTCAGCTGCTGCCATGTTGGCAAGCGCAGGAGTA 523
DB 117 GACTGCCATCGCTTCGCGTGCTTTACCGCGCGGCCATGTTGGCCAGCGCAGGAGTA 176
QY 524 CTTGTACCTCGGGGGCTTCTTTTCATCTGGCGTCTCCCTCTCTCTTCTGCTTGCCTTGC 583
DB 177 CTTCTACCTGGGTGGCTGCTCTCGTGGGGCTCTCCATCTGCTCTGCTGACGTAGC 236
QY 584 ATCTCCATTTTGGTGGTTCATGCTGTTTCAAGTTGAGTTGATTTGGACTCTT 643
DB 237 CGGCTCCATCTTCGGCACTCCGCAACCAAGCTCATGTTGAGGCTTACTTCGGGCTGCT 296
QY 644 GGTGTTTGTGGGCTACATCTCTTTGACACCCCAAGAAATTTAGAAAGGCTCACTTGGG 703
DB 297 CATCTTCCTGGCTACGTGTTGACGACGCGGAGATCATCGAGAGGCGCACCGCGG 356
QY 704 TGATATGATGATTAGTAAAGCATGATGACCTTTTCACAGATTTTGGCGCTGTTTGT 763
DB 357 CGACATGGACACGTCAGCAGCACCCCTCACCCTCTTTCACAGACTTCGTGGCGCTCCTGT 416
QY 764 GCGGATTCATCATCATGTTAAAGATGATCATCTGAGAAGGAGAGAGAGAGAGAG 823
DB 417 CCGGCTCTCTCATCATGCTCAGAACGGGCGCAGCAAGTCGGAGGACAGAGAGGA 476
QY 824 GA 825
DB 477 GA 478
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```

RESULT 15
US-10-167-015-22
; Sequence 22, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Jehal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
```

```

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 308
; TYPE: DNA
; ORGANISM: glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(308)
; OTHER INFORMATION: n = A,T,C or G
US-10-167-015-22

Query Match      17.2%; Score 177.8; DB 9; Length 308;
Best Local Similarity 75.6%; Pred. No. 2.4e-45;
Matches 232; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 453 GCTTTTGTAGTTGTGCTGTTGTTTGGTTGCTTCTCAGCTGCTGCCATGTTGGCAAGG 512
DB 2 GCATTTGTGGGAACATCCTTGGCCTTTTGCATGCTTCTCAGAGCAGCTTTGGTTGCTAGG 61
QY 513 CGCAGGGAGTACTTGTACTCGGGGGCTTCTTTTCATCTGGCGTCTCCCTTCTCTCTG 572
DB 62 CGTAGGGAGTACTTGTACTTGGTGGCTTGTCTTCTGATTGTCATCCTTCTCTG 121
QY 573 TTGCACTTGTGATCCTCCATTTTGGTGGTTCATGGCTGTTTTCAGTTTGTAT 632
DB 122 TTGCACCTTGTCTTCTCCATCTTTGGAGGTTCAACAGCTCTCTTTAAAGTTGAGTTGTAC 181
QY 633 TTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCC -AAGAAATTTAGAA 691
DB 182 TTTGGCTTTTGGTGTGTTGGTATGATTACATTAGTACACCCCAAGAAATAGTTGAGAN 241
QY 692 GGCTCACTTGGGTGATGATGATTAGTTAAGTAAAGCATGCAATGACCTTTTTCAGATTTGG 751
DB 242 GGCACACTTGGGCGATCTGGACTATGTAAGCATGCCCTTGACCTTGTTTACCGATTTG 301
QY 752 CGCTGTT 758
DB 302 TGCATTT 308
```

Search completed: May 25, 2003, 12:19:38  
Job time : 170 secs

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 09:52:48 ; Search time 1487 Seconds  
(without alignments)

11261.690 Million cell updates/sec

Title: US-09-955-526-3

Perfect score: 1034

Sequence: 1 ggcgaacataacattgtct.....ataaggaagttccttgta 1034

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_esti:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	717	69.3	750	12	BG124317
2	647.4	62.6	671	13	BI933489
3	643	62.2	643	10	AW096641
4	634	61.3	645	10	AW219279
5	621.8	60.1	647	12	BG127849
6	596	57.6	596	9	AI779122

7	591	57.2	592	12	BG134507
8	534.2	51.7	578	14	BQ115430
9	498.4	48.2	540	12	BF054243
10	468.8	45.3	476	13	BI935239
11	454.4	43.9	464	9	AI895377
12	449.2	43.4	617	14	BQ115431
13	437.8	42.3	456	9	AI776541
14	423	40.9	448	10	AW399750
15	422	40.8	488	12	BE919556
16	417.6	40.4	831	12	EG839316
17	416.8	40.3	424	10	AW912823
18	416.4	40.3	464	10	AW617419
19	412	39.8	428	10	AW399749
20	405	39.2	732	14	BQ023368
21	384.2	37.2	713	14	BQ991270
22	379.4	36.7	694	12	BQ646982
23	378.8	36.6	723	14	BQ856331
24	376.4	36.4	703	14	BQ863266
25	374.8	36.2	726	12	BQ648712
26	364.4	35.2	740	14	BQ255427
27	356.6	34.5	647	10	BE577220
28	350.8	33.9	847	14	BQ792694
29	348.2	33.7	681	12	BF635314
30	343.8	33.2	776	12	BQ648573
31	338.8	32.8	752	12	BQ647209
32	337.8	32.7	643	14	BQ401834
33	337.8	32.7	811	14	BQ165367
34	335.4	32.4	620	9	AI730983
35	335	32.4	621	9	AI726851
36	334.4	32.3	619	9	AI727198
37	331.4	32.1	525	9	AJ412594
38	324.6	31.4	595	9	AI166999
39	321.4	31.1	548	12	BF423787
40	320.4	31.0	391	9	AI780552
41	312.4	30.2	621	9	AI731928
42	312	30.2	978	11	AY107681
43	310.6	30.0	665	14	BQ246217
44	309.6	29.9	761	14	BQ165368
45	307.8	29.8	551	10	AW323256

ALIGNMENTS

RESULT 1  
BG124317  
LOCUS  
DEFINITION  
EST469963 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
ctof4l8 5' sequence, mRNA sequence.  
ACCESSION  
BG124317.1 GI:12624505  
VERSION  
KEYWORDS  
EST.  
SOURCE  
tomato.  
ORGANISM  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

750 bp mRNA linear EST 31-JAN-2001  
tomato shoot/meristem Lycopersicon esculentum cDNA clone  
5' sequence, mRNA sequence.

REFERENCE  
AUTHORS  
Hansen, C., Rønning, C. and Tanksley, S.  
TITLE  
Generation of ESTs from tomato shoot/meristem tissue  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES  
source  
1..750  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"

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/clone="ctof418"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/notes="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT      158 a 174 c 176 g 242 t
ORIGIN
Query Match      69.3%; Score 717; DB 12; Length 750;
Best Local Similarity 98.9%; Pred. No. 4.1e-173;
Matches 733; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
QY 2 AGCAACATACATTTGCTAGCTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAAA 61
DB 10 AGCAACATACATTTGCTAGCTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAAA 69
QY 62 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
DB 70 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
QY 122 TGCCTCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAATTCGCCAGATCTCACCTCT 181
DB 130 TGCCTCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAATTCGCCAGATCTCACCTCT 189
QY 182 CGTTCAATCTCTCAAGCAGGTGACCTTACGCTATGCTGTGCTTTAGTGGCATCGGC 241
DB 190 CGTTCAATCTCTCAAGCAGGTGACCTTACGCTATGCTGTGCTTTAGTGGCATCGGC 249
QY 242 TGCCTGGGCTTACCTTCAATCTATGGAATATCGTGGCTCTCTCAAAATTCGCCAGT 301
DB 250 TGCCTGGGCTTACCTTCAATCTATGGAATATCGTGGCTCTCTCAAAATTCGCCAGT 309
QY 302 CATGGAAGAGAGTGTGTGCTCTCAGCTCTCTCTATCAG---AGCAAAAAGGT 358
DB 310 CATGGAAGAGAGTGTGTGCTCTCAGCTCTCTCTATCAGAGAGAGAGAGAGAGAGGT 369
QY 359 GGCTCTTCTGATGGCAGCTGCATTTTTCAGCGCGCTCTATTGGTCTCTGATTGAGCT 418
DB 370 GGCTCTTCTGATGGCAGCTGCATTTTTCAGCGCGCTCTATTGGTCTCTGATTGAGCT 429
QY 419 GGGCATTAATCTCGATCCAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTTT 478
DB 430 GGGCATTAATCTCGATCCAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTTT 489
QY 479 TGGTGTCTTCTAGCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCTGGGG 538
DB 490 TGGTGTCTTCTAGCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCTGGGG 549
QY 539 CCTTCTTTTCTAGCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCTGGGG 598
DB 550 CCTTCTTTTCTAGCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCTGGGG 609
QY 599 TGGTTCATGCTGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTT 658
DB 610 TGGTTCATGCTGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTTTCAGTTT 669
QY 659 CATCGCTTTTGACACCCAGAGAAATTTAGAGAGGCTCTCTTGGGTGATATGATATCGT 718
DB 670 CATCGCTTTTGACACCCAGAGAAATTTAGAGAGGCTCTCTTGGGTGATATGATATCGT 729
QY 719 TAAGCATGCAATGACCCCTTTT 739
DB 730 TAAGCATGCAATGACCCCTTTT 750

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RESULT 2  
 B1933489 671 bp mRNA linear EST 18-OCT-2001  
 LOCUS B1933489  
 DEFINITION EST553378 tomato flower, anthesis Lycopersicon esculentum cDNA

```

clone cTOD16N14 5' end, mRNA sequence.
B1933489
VERSION B1933489.1 GI:16247961
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 671)
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Uteback,T., Van Aken,S., Rinning,C.M., Nierman,W., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute.
Seq primer: T3.
Location/Qualifiers
1..671
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOD16N14"
/clone_lib="tomato flower, anthesis"
/tissue_type="flower"
/dev_stage="anthesis"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT      134 a 161 c 157 g 219 t
ORIGIN
Query Match      62.6%; Score 647.4; DB 13; Length 671;
Best Local Similarity 99.6%; Pred. No. 2.9e-155;
Matches 570; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 12 ACATTGTCTACGTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAACTCGAAGAG 71
DB 1 ACATTGTCTACGTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAACTCGAAGAG 60
QY 72 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131
DB 61 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 132 AACCGTGGAGTTATGATTTCTCTCAAAATTCGCCAGATCTCACCTCTCGTTCAAAC 191
DB 121 AACCGTGGAGTTATGATTTCTCTCAAAATTCGCCAGATCTCACCTCTCGTTCAAAC 180
QY 192 CATCTCAAGCAGGTGACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGTGGGGCT 251
DB 181 CATCTCAAGCAGGTGACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGTGGGGCT 240
QY 252 TACCTTCAATTTTGAATATCGTGGCTCTCTCAACAANTGGCTTCGATGGGAGC 311
DB 241 TACCTTCAATTTTGAATATCGTGGCTCTCTCAACAANTGGCTTCGATGGGAGC 300
QY 312 ATGGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTCTGATG 371
DB 301 ATGGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTCTGATG 360
QY 372 GCAGCTGCATTTTGAAGGCGCTCTATTGGTCTCTGATGAGCTGGGCAATTAATTC 431
DB 361 GCAGCTGCATTTTGAAGGCGCTCTATTGGTCTCTGATGAGCTGGGCAATTAATTC 420

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QY 432 GATCCAGCAATGTTGGCGCTTTTGTAGGTTGCTGTGTTTGGTGTCTCTCA 491  
Db 421 GATCCAGCAATGTTGGCGCTTTTGTAGGTTGCTGTGTTTGGTGTCTCTCA 480  
QY 492 GCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCGGGGCTCTTTCATCT 551  
Db 481 GCTGCTGCCATGTTGCAAGGCGCAGGAGTACTTGTACTCGGGGCTCTTTCATCT 540  
QY 552 GGGCTCTCCCTTCTCTTCTGTTGCACTTTGTCATCTCCATTTTGGTGTCCATGGCT 611  
Db 541 GGGCTCTCCCTTCTCTTCTGTTGCACTTTGTCATCTCCATTTTGGT-GTTCATGGCT 599  
QY 612 GTTTTCAAGTTGAGTTGATTTTGAACCTTGGTGTGTTGCTGAGTACATCTCTTTGAC 671  
Db 600 GTTTTCAAG-TTGAGTTGATTTTGGACTCTTGGTGGTGTGCTGAGTACATCTCTTTGAC 658  
QY 672 ACCCAAGAAATTA 684  
Db 659 ACCCAAGAAATTA 671

RESULT 3  
AW096641  
LOCUS  
DEFINITION EST29821 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA  
ACCESSION AW096641 643 bp mRNA linear EST 18-MAY-2001  
VERSION AW096641.1 GI:6062236  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

REFERENCE  
1 (bases 1 to 643)  
D'Asenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,  
Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,  
Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni  
J.  
Generation of ESTs from tomato leaf tissue  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
Location/Qualifiers  
1. 643  
/organism="Lycopersicon esculentum"  
/cultivar="Rio Grande PtoR"  
/db\_xref="taxon:4081"  
/clone="cLET39M7"  
/clone\_lib="tomato mixed elicitor, BTI"  
/tissue\_type="leaf"  
/dev\_stage="4-6 week old plants"  
/lab\_host="XLI-Blue MRF"  
/note="vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:  
XhoI; cLET - inoculated with a variety of disease response  
elicitors. Plants exposed to 2,6 dichloroisonicotinic  
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,  
okadaic acid, or systemin prior to tissue harvest. EcoRI  
site was destroyed during cloning."  
BASE COUNT 129 a 155 c 150 g 209 t  
ORIGIN  
Query Match 62.2%; Score 643; DB 10; Length 643;  
Best Local Similarity 100.0%; Pred. No. 3.8e-154;  
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAACATACATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCCAGTTCCAAAAC 62

Db 1 GCAACATACATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCCAGTTCCAAAAC 60  
QY 63 TCGAAGAAGAAGAAGAACAATGGAAGTTTCACATCGTTCTTCGACTCGCAATCT 122  
Db 61 TCGAAGAAGAAGAAGAACAATGGAAGTTTCACATCGTTCTTCGACTCGCAATCT 120  
QY 123 GCTCTCGCAACGGCTGGAGTTATGATTTCTCAAAAACATTCGCCAGATCTCACCTCTC 182  
Db 121 GCTCTCGCAACGGCTGGAGTTATGATTTCTCAAAAACATTCGCCAGATCTCACCTCTC 180  
QY 183 GTTCAAACTCATCTCAAGCAGGTGTACCTTAGCTATACCTGTGCTTTAGTGGCATCGGCT 242  
Db 181 GTTCAAACTCATCTCAAGCAGGTGTACCTTAGCTATACCTGTGCTTTAGTGGCATCGGCT 240  
QY 243 GCTGGGCTTACCTTCAATTCATGGAATATCGTGAGCTCTCTCAACAATGGCTTGC 302  
Db 241 GCTGGGCTTACCTTCAATTCATGGAATATCGTGAGCTCTCTCAACAATGGCTTGC 300  
QY 303 ATGGGAAGCATGTTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGTTGGCT 362  
Db 301 ATGGGAAGCATGTTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGTTGGCT 360  
QY 363 CTCTCATGGCAGCTGCACCTTTTGAAGCGCTCTATGTCCTCTGATTCAGTGGGCT 422  
Db 361 CTCTCATGGCAGCTGCACCTTTTGAAGCGCTCTATGTCCTCTGATTCAGTGGGCT 420  
QY 423 ATTAACCTTCGATCCAGCATGTTGTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGT 482  
Db 421 ATTAACCTTCGATCCAGCATGTTGTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGT 480  
QY 483 TGCTTCTCAGCTGCTCCCAATGTTGGCAAGCGCGCAGTACTTGTACTCGGGGCTTT 542  
Db 481 TGCTTCTCAGCTGCTCCCAATGTTGGCAAGCGCGCAGTACTTGTACTCGGGGCTTT 540  
QY 543 CTCTCATCTGGGCTCTCCCTCTCTCTCGTTGCACTTTGATCTCTCCATTTTGGTGGT 602  
Db 541 CTCTCATCTGGGCTCTCCCTCTCTCTCGTTGCACTTTGATCTCTCCATTTTGGTGGT 600  
QY 603 TCCATGGCTGTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 645  
Db 601 TCCATGGCTGTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 643

RESULT 4  
AW219279  
LOCUS  
DEFINITION EST301761 tomato root during/after fruit set, Cornell University  
ACCESSION AW219279 646 bp mRNA linear EST 18-MAY-2001  
VERSION AW219279  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

REFERENCE  
1 (bases 1 to 646)  
van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Liang, F.,  
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,  
Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
Generation of ESTs from tomato root tissue  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
Location/Qualifiers  
1. 646  
/organism="Lycopersicon esculentum"







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QY 63 TCGAAGAAAGAAAGAGAGAAACAATGGAAGGTTTCACATGTTCTTCGACTCGCAATCT 122
DB 61 TCGAAGAAAGAAAGAGAGAGAAACAATGGAAGGTTTCACATGTTCTTCGACTCGCAATCT 120
QY 123 GCCTCTCGCAACCGGTGAGATGATGATCTCTCAAAACTTCGCCAGATCTCACCTCTC 182
DB 121 GCCTCTCGCAACCGGTGAGATGATGATCTCTCAAAACTTCGCCAGATCTCACCTCTC 180
QY 183 GTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCT 242
DB 181 GTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCT 240
QY 243 GTGGGGCTTACCTTCAATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTC 302
DB 241 GTGGGGCTTACCTTCAATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTC 300
QY 303 ATGGGAAGCATGGTGTGCTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCT 362
DB 301 ATGGGAAGCATGGTGTGCTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCT 360
QY 363 CTTCTGATGGAGCTGCACTTTTGAAGGGGCTCTATGCTCTCTGATGAGCTGGGC 422
DB 361 CTTCTGATGGAGCTGCACTTTTGAAGGGGCTCTATGCTCTCTGATGAGCTGGGC 420
QY 423 ATTAATCTCGATCCAGCAATGCTGTTGGCGCTTTTGTAGCTGTGCTGTGTTTGGT 482
DB 421 ATTAATCTCGATCCAGCAATGCTGTTGGCGCTTTTGTAGCTGTGCTGTGTTTGGT 480
QY 483 TGGCTTCAAGCTGCTGCCATGTTGCAAGGGCGCAGGAGTACTTGTACCTCGGGGGCTT 542
DB 481 TGGCTTCAAGCTGCTGCCATGTTGCAAGGGCGCAGGAGTACTTGTACCTCGGGGGCTT 540
QY 543 CTTTCACTTGGGGTCTCCCTCTCTCTGTTGTCATTTGATCTCTCATTT 594
DB 541 CTTTCACTTGGGGTCTCCCTCTCTCTGTTGTCATTTGATCTCTCATTT 592

```

```

RESULT 8
LOCUS BQ115430 578 bp mRNA linear EST 22-JUL-2002
DEFINITION EST600993 mixed potato tissues Solanum tuberosum cDNA clone STMDA93
5' end, mRNA sequence.

```

```

ACCESSION BQ115430
VERSION BQ115430.2 GI:21916950
KEYWORDS EST.
SOURCE potato.

```

## ORGANISM

```

Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20167379.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@igr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cnaresgen.com
Seq primer: 13.

```

```

FEATURES
source

```

```

Location/Qualifiers
1..578
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjite"
/db_xref="taxon:4113"
/clone="STMDA93"
/clone_lib="mixed potato tissues"
/tissue_type="mixed tissues"

```

```

/lab_host="SOLR"

```

```

/Note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

```

```

BASE COUNT 117 a 140 c 137 g 184 t
ORIGIN

```

```

Query Match 51.7%; Score 534.2; DB 14; Length 578;
Best Local Similarity 96.5%; Pred. No. 3e-126;
Matches 557; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

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```

QY 11 AACATCTCTACGTTACAGATAAATATCCTTTGCTCATTTTCAGTTCCTCAAAAACCTCGAAGAA 70
DB 4 AACATTTGTACGTTACAGATAAATATCCTTTGCTCATTTTCAGTTCCTCAAAAACCTCGAAGAA 63

```

```

QY 71 GAAGAAGAAGAGAAACAATGGAAGGTTTCACATGTTCTTCGACTCGCAATCTCGCTCTCG 130
DB 64 GAAGAAGA--AGAATAATGAGGGTTTCACATGTTCTTCGACTCGCAATCTCGCTCTCG 121

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```

QY 131 CAACGGCTGGAGTTATCATTTCTCAAAAACCTTCGCCAGATCTCACCTCTCGTTCAAAAC 190
DB 122 CAACGGCTGGAGTTATCATTTCTCAAGAATCTTCGCCAGATCTCACCTCTCGTTCAAAAC 181

```

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QY 191 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTTAGTGGCATCGGCTCGTGGGC 250
DB 182 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTTAGTGGCATCGGCTCGTGGGC 241

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QY 251 TTACCTTCACATTTCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTGCAATGGGAAG 310
DB 242 TTACCTTCACATTTCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTGCAATGGGAAG 301

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QY 311 CATGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGAT 370
DB 302 CATGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGAT 361

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QY 371 GCAGCTGCATTTTGAAGGGCTCTATTTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
DB 362 GCAGCTGCATTTTGAAGGGCTCTATTTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421

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```

QY 431 CGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
DB 422 CGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481

```

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QY 491 AGCTGCTGCATTTGGAAGGGCGCAGGAGTACTTCTACCTCGGGGGCTTCTTTTCATC 550
DB 482 AGCTGCTGCATTTGGAAGGGCGCAGGAGTACTTCTACCTCGGGGGCTTCTTTTCATC 541

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QY 551 TGGCGTCTCCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
DB 542 TGGCGTCTCCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578

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RESULT 9
BF054243 540 bp mRNA linear EST 16-OCT-2000
LOCUS EST439473 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION CSTB39K21 5' sequence, mRNA sequence.

```

```

ACCESSION BF054243
VERSION BF054243.1 GI:10808139
KEYWORDS EST.
SOURCE potato.

```

```

ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Rønning,
C.M., Fry, W.B., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)

```

## COMMENT

Contact: Cathy Romning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com.  
Location/Qualifiers

## FEATURES

source  
1. .540  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db xref="taxon:4113"  
/clone="cSTB39K21"  
/clone\_lib="potato leaves and petioles"  
/tissue\_type="leaflets and petioles"  
/dev\_stage="8 weeks old plants"  
/lab\_host="SOLR"  
/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Tissue was supplied by Dr. Fry (Cornell University).  
Leaflets and petioles were isolated from 8 week old  
greenhouse grown plants. The plants were watered and  
fertilized freely. The tissue was immediately frozen in  
liquid nitrogen."

BASE COUNT 114 a 127 c 130 g 169 t  
ORIGIN

Query Match 48.2%; Score 498.4; DB 12; Length 540;  
Best Local Similarity 96.5%; Pred. No. 4.5e-117;  
Matches 521; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

Qy 11 AACATGTCTAGTTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAACTCGAAGAA 70  
Db 4 AACATGTGTAGCTTCAGATAAATATCCTTTGCTCGTTTCAGTTCGAAAACTC---GAA 60  
Qy 71 GAAGAAGAAGACAAATGGAAGGTTTCACATCGTTCTTCGATCGCAATCGCCCTCTCG 130  
Db 61 GAAGAAGAAGATATGAGAGGTTTCACATCGTTCTTCGATCGCAATCGCCCTCTCG 120  
Qy 131 CAACGCTGGAGTTATGATTTCTTCAAAAACCTCCGCGAGATCTCACTCTGTTCAAAAC 190  
Db 121 CAACGCTGGAGTTATGATTTCTTCAAAAACCTCCGCGAGATCTCACTCTGTTCAAAAC 180  
Qy 191 TCATCTCAAGCAGGTGTACCTTACGATGCTGTGCTTTAGTGGCATCGGCTCTCGGCG 250  
Db 181 TCATCTCAAGCAGGTGTACCTTACGATGCTGTGCTTTAGTGGCATCGGCTCTCGGCG 240  
Qy 251 TTACCTTCAATTCATGGAATATCGGTGGCTCTCTCAACAATGCTTGCATGGGAAG 310  
Db 241 TTACCTTCAATTCATGGAATATCGGTGGCTCTCTCAACAATGCTTGCATGGGAAG 300  
Qy 311 CATGTTGGCTTCTCTCAGCTCCTCTTATCAAGACAAAGAGGTTGCTCTCTGAT 370  
Db 301 CATGTTGGCTTCTCTCAGCTCCTCTTATCAAGACAAAGAGGTTGCTCTCTGAT 360  
Qy 371 GCGAGCTGCATTTTGAAGCGCTCTATTTGGTCTCTGATTTGAGTGGGCATTAACCT 430  
Db 361 GCGAGCTGCATTTTGAAGCGCTTCTATTTGGTCTCTGATTTGAGTGGGCATTAACCT 420  
Qy 431 CGATCCAGCATTTGTTGGCGCTTTTGGAGTTGCTGTGTTGGTTTGGTTGCTCTC 490  
Db 421 CGATCCAGCATTTGTTGGCGCTTTTGGAGTTGCTGTGTTGGTTTGGTTGCTCTC 480  
Qy 491 AGCTGCTGCCATTTGGCAAGCGCAGGAGTACTTGTACTCTGGGGGCTCTCTTTCATC 550  
Db 481 AGCTGCTGCCATTTGGCAAGCGTGGAGTACTTGTACTCTGGGGGCTCTCTTTCATC 540

## RESULT 10

BI935239

LOCUS

EST55128 tomato flower, anthesis Lycopersicon esculentum cDNA

DEFINITION clone cTOD22C8 5' end, mRNA sequence.

ACCESSION BI935239

VERSION BI935239.1 GI:16249711

KEYWORDS EST.

SOURCE tomato.

## ORGANISM

Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 476)

## REFERENCE

## AUTHORS

van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,  
Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,  
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

## TITLE

## JOURNAL

## COMMENT

Generation of ESTs from tomato flower tissue, anthesis (2001)  
Unpublished (2001)

Contact: CUGI  
Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3

Location/Qualifiers

1. .476

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db xref="taxon:4081"

/clone="cTOD22C8"

/clone\_lib="tomato flower, anthesis"

/tissue\_type="flower"

/dev\_stage="anthesis"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; supplier: Cornell University; sequencing: The  
Institute for Genomic Research; Flower buds and flowers  
were taken from greenhouse plants (4-8 wks old, TA496).  
They were immediately frozen in liquid nitrogen and then  
size-separated while remaining frozen."

BASE COUNT 114 a 115 c 106 g 141 t

## ORIGIN

Query Match 45.3%; Score 468.8; DB 13; Length 476;  
Best Local Similarity 99.6%; Pred. No. 1.7e-109;  
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCAACATACATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAAA 61  
Db 5 AGCAACATACATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAAA 64  
Qy 62 CTCGAAGAAGAAGAGACAAATGGAAGTTTCACATCGTTCTTCGACTCGCAATC 121  
Db 65 CTCGAAGAAGAAGAGACAAATGGAAGTTTCACATCGTTCTTCGACTCGCAATC 124  
Qy 122 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCGCAGATCTCACCTCT 181  
Db 125 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCGCAGATCTCACCTCT 184  
Qy 182 CGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTAGTGGCATCGGC 241  
Db 185 CGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTAGTGGCATCGGC 244  
Qy 242 TGCCTGGGCTTACCTTCACATTCATGGAATATCGGTGGCTTCCTCAACAATGGCTTG 301  
Db 245 TGCCTGGGCTTACCTTCACATTCATGGAATATCGGTGGCTTCCTCAACAATGGCTTG 304  
Qy 302 CATGGGAAGCATGGTGTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGTTGCG 361  
Db 305 CATGGGAAGCATGGTGTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGTTGCG 364  
Qy 362 TCTTCTCATGGCAGCTGCACCTTTTGAAGCGCGCTCTATTGGTCTCTGATTGAGCTGGG 421  
Db 365 TCTTCTCATGGCAGCTGCACCTTTTGAAGCGCGCTCTATTGGTCTCTGATTGAGCTGGG 424  
Qy 422 CATTAACCTTCATCCAGCATTTGTTGGCGCTTTTGTAGTGTGCTGTG 473  
Db 425 CATTAACCTTCATCCAGCATTTGTTGGCGCTTTTGTAGTGTGCTGTG 476

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RESULT 11
AI895377      464 bp  mRNA  linear  EST 18-MAY-2001
LOCUS        TAMU Lycopersicon esculentum cDNA clone
DEFINITION   EST264820 tomato callus, TAMU Lycopersicon esculentum cDNA clone
ACCESSION   CLC7H19, mRNA sequence.
VERSION     AI895377
KEYWORDS    AI895377.1 GI:5601279
SOURCE      EST.
ORGANISM    tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 464)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ann, S., Romling,
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES             source
Location/Qualifiers
1..464
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; CLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
BASE COUNT          99 a 112 c 116 g 137 t
ORIGIN
Query Match          43.9%; Score 454.4; DB 9; Length 464;
Best Local Similarity 98.7%; Pred. No. 8.3e-106;
Matches 458; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 62 CTCGAGAGAGAGAGAGAGACATGAGGTTTCATCGTTCTTCGACTCGCAATC 121
DB 1 CTCGAGAGAGAGAGAGAGATCAATGAGGTTTCATCGTTCTTCGACTCGCAATC 60
QY 122 TGCCTCTCGCAACCGTGGAGTATGATCTCTCAAAACCTTCGCCAGACTCACCTCT 181
DB 61 TGCCTCTCGCAACCGTGGAGTATGATCTCTCAAAACCTTCGCCAGACTCACCTCT 120
QY 182 CGTTCAAACCTCATCTCAAGCAGGTGTACCTTACGCTATCGTGTCTTTAGTGGCATCGGC 241
DB 121 CGTTCAAACCTCATCTCAAGCAGGTGTACCTTACGCTATCGTGTCTTTAGTGGCATCGGC 180
QY 242 TGTGGGGCTTACCTTCACATTCATGGAATATCGGTGGCTCTCTCAACAAGTGGCTTG 301
DB 181 TGTGGGGCTTACCTTCACATTCATGGAATATCGGTGGCTCTCTCAACAAGTGGCTTG 240
QY 302 CATGGGAAGCATGTTGGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGC 361
DB 241 CATGGGAAGCATGTTGGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGC 300
QY 362 TCCTCTCATGGCAGCTGCACCTTTTGAAGCGGCTCTATGTGCTCTCATGAGCTGGG 421
DB 301 TCCTCTCATGGCAGCTGCACCTTTTGAAGCGGCTCTATGTGCTCTCATGAGCTGGG 360

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QY 422 CATTAACTTCGATCCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGTGCTGTGTTTGG 481
DB 361 CATTAATTCGATCCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGTGCTGTGTTTGG 420
QY 482 TTGCTTCTCAGCTGCTGCCATGTGTGCAAGGCGCAGGAGTACT 525
DB 421 TTGCTTCTCAACTGCTGGCATGTGTGCAAGGCGCAGGAGTACT 464

RESULT 12
BQ115431/c 617 bp  mRNA  linear  EST 17-APR-2002
LOCUS      EST600994 mixed potato tissues Solanum tuberosum cDNA clone STMDA93
DEFINITION 3' end, mRNA sequence.
ACCESSION  BQ115431
VERSION    BQ115431.1 GI:20167380
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 617)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karanycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@igr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T7.
FEATURES             Location/Qualifiers
source              1..617
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjite"
/db_xref="taxon:4113"
/clone="STMDA93"
/clone_lib="mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
, tubers, or roots."
BASE COUNT          219 a 152 c 114 g 132 t
ORIGIN
Query Match          43.4%; Score 449.2; DB 14; Length 617;
Best Local Similarity 89.9%; Pred. No. 1.9e-104;
Matches 524; Conservative 0; Mismatches 34; Indels 25; Gaps 3;
QY 402 GGTCTCTGATGAGCTGGCATTAACTTCATCTTCAGCTGTGCCAAGCGCGTTTGT 460
DB 617 GGTCTCTGATGAGCTGGCATTAACTTCATCTTCAGCTGTGCCAAGCGCGTTTGT 558
QY 461 AGTTGTGTGTGGTGTGTTTGTGTTGTTCTCAGCTGTGCCAAGCGCGCGGGA 520
DB 557 AGTTGTGTGTGGTGTGTTTGTGTTGTTCTCAGCTGTGCCAAGCGCGTAGGGA 498
QY 521 GTACTTGTACCTCGGGGGCTCTTTCATCTGCGGTCTCCCTCTCTCTGTTGCACTT 580
DB 497 GTACTTGTACCTCGGGGGCTCTTTCATCTGCGGTCTCCCTCTCTCTGTTGCACTT 438
QY 581 TGCATCTCCTCACTTTTGTGGTTCATCGCTGTTTCAAGTTTCAGTTGATTTTGAAT 640
DB 437 CGCATCTCCATTTTGTGGTTCATCGCTGTTTCAAGTTTCAGTTGATTTTGAAT 378

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QY 641 CTTGGTGTGTTGGGCTACATGCTCTTGGACCCCAAGAAATATTGAGAGGCTCACTT 700
DB 377 CTTGGTGTGTTGGGCTACATGCTCTTGGACCCCAAGAAATATTGAGAGGCTCACTT 318
QY 701 GGGTCAATAGGATTACGTTAAGCATGCAATGACCTTTTTCACAGATTTTGGCGCTGTTTT 760
DB 317 GGGTCAATAGGACTACGTTAAGCATGCTTTGACCTCTTTCACAGATTTTGGCTGTTTT 258
QY 761 TGTGCGGATCTGATCATCATGTTAAAGTAATGATCTGAGAGGAGAGAGAGAGAA 820
DB 257 TGTGCGGATCTGATCATCATGTTAAAGTAATGATCTGAGAGGAGAGAGAGAGAA 198
QY 821 GAGGAGAACTAGATTGCTTCT- 861
DB 197 GAGGAGAACTAGATTGCTTCTATGGGCTACTGGGACTCTAACCTGTGTTTCATA 138
QY 862 ACTCCCTGTGTTCACTGAAACAGCATGTTAATAGTTGATCTTCTTCACTTTAGCA 921
DB 137 ATACACTGTGTTCACTGAAACAGCATGTTAATAGTTGATCTTCTTCACTTTAGCA 83
QY 922 TAGGCTGTGATGTAATGCTGTGACATGCCATTATGGCTGTG 964
DB 82 TTGGCTGTGATACATAATGCTGGCATGCCATTATGGCTGTG 40

RESULT 13
AI776541 456 bp mRNA linear EST 18-MAY-2001
LOCUS EST257641 tomato resistant, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLER18J18, mRNA sequence.
ACCESSION AI776541
VERSION AI776541
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 456)
AUTHORS D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
TITLE Generation of ESTs from Pseudomonas resistant tomato
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
    source
        1..456
            /organism="Lycopersicon esculentum"
            /cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
            /db_xref="taxon:4081"
            /clone="cLER18J18"
            /clone_lib="tomato resistant, Cornell"
            /tissue_type="leaf"
            /dev_stage="4-week old"
            /lab_host="SOLR"
    note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; cLER - Tomato Pseudomonas Resistant EST Library_
Directionally cloned cDNAs inserted into pBluescript SK(-)
) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 103 a 114 c 102 g 137 t
ORIGIN
    Query Match 42.3%; Score 437.8; DB 9; Length 456;
    Best Local Similarity 99.3%; Pred. No. 1.5e-101;
    Matches 450; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 19 CTACGTTGAGATAAATATCCCTTTGCTCAATTTTCAGTTCCAAAACTCGAAGAGAGA 78
DB 4 CTACGTTGAGATAAATATCCCTTTGCTCAATTTTCAGTTCCAAAACTCGAAGAGAGA 63
QY 79 AGAGAACAAATGAAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCAACGGCT 138
DB 64 AGAGAACAAATGAAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCCTCTCGCAACGGCT 123
QY 139 GGAGTTATGATTCTCTCAAAAACTTCGCGCAGATCTCACCTCTCGTTCAAACTCATCTCA 198
DB 124 GGAGTTATGATTCTCTCAAAAACTTCGCGCAGATCTCACCTCTCGTTCAAACTCATCTCA 183
QY 199 AGCAGGTGTACCTTACGCTAATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTC 258
DB 184 AGCAGGTGTACCTTACGCTAATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTC 243
QY 259 ACATTTATGGAATATCGTGGCTCTCTCAACAATGGCTTGATGGGAAGCATGGTGT 318
DB 244 ACATTTATGGAATATCGTGGCTCTCTCAACAATGGCTTGATGGGAAGCATGGTGT 303
QY 319 GGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAAGGCTGCTCTTCTGATGGCAGCTG 378
DB 304 GGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAAGGCTGCTCTTCTGATGGCAGCTG 363
QY 379 CACTTTTGAAGGCG-CTCTATTTGGTCTCTGATTTAGCTGGGCAATTAACCTGATCCA 437
DB 364 CACTTTTGAAGGCGCTCTATTTGGTCTCTGATTTAGCTGGGCAATTAACCTGATCCA 423
QY 438 AGCATTGTGTTTGGCGCTTTTGTAGTGTGCT 470
DB 424 AGCATTGTGTTTGGCGCTTTTGTAGTGTGCT 456

RESULT 14
AW399750 448 bp mRNA linear EST 18-MAY-2001
LOCUS EST310250 L. pennellii trichome, Cornell University Lycopersicon
DEFINITION pennellii cDNA clone cJPT8N10 5', mRNA sequence.
ACCESSION AW399750
VERSION AW399750
KEYWORDS EST.
SOURCE Lycopersicon pennellii.
ORGANISM Lycopersicon pennellii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 448)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii
C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
G.B., Tanksley,S.D. and Giovannoni,J.
TITLE Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
    source
        1..448
            /organism="Lycopersicon pennellii"
            /db_xref="taxon:28526"
            /clone="cJPT8N10"
            /clone_lib="L. pennellii trichome, Cornell University"
            /tissue_type="trichome"
            /dev_stage="mixed stages"
            /lab_host="SOLR"
    note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Leaves of various stages were shaken in liquid

```

nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."

BASE COUNT 107 a 112 c 98 g 131 t  
ORIGIN

Query Match 40.9%; Score 423; DB 10; Length 448;  
Best Local Similarity 96.6%; Pred. No. 9.3e-98;  
Matches 432; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 10 TAACATGCTACGTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAACCTCGAAGA 69  
Db 2 TATTATTGCTACGTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAACCTCGAAGA 61  
QY 70 AGAAGAAGAGAGACAATGGAAGTTTACATGCTTTCGACTCCCAATTCGCTCTC 129  
Db 62 AGAAGAAGAGAGACAATGGAAGTTTACATGCTTTCGACTCCCAATTCGCTCTC 121  
QY 130 GCAACCGCTGGAGTTATGATTTCTCAAAAACCTTCGCGCAGATCTCACTCTCGTTCAAA 189  
Db 122 GCAACCGCTGGAGTTATGATTTCTCAAAAACCTTCGCGCAGATCTCACTCTCGTTCAAA 181  
QY 190 CTCATCTCAAGCAGGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGGGG 249  
Db 182 CTCATCTCAAGCAGGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGGAGGG 241  
QY 250 CTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATGGAA 309  
Db 242 CTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATGGAA 301  
QY 310 GCATGCTGGCTTCTCTCAGTCTCTCTCTATPCAGAGCAAAAAGGGTGGCTCTCTCTGA 369  
Db 302 GCATGATGAGGCTTCTCTCAACTCTCTCTATPCAGAGCAAAAAGGGTGGCTCTCTCTGA 361  
QY 370 TGGCAGCTGCACCTTTTGAAGCGCTCTATTTGGTCTCTCTGATTCAGCTGGGCATTAACT 429  
Db 362 TGGCAGCTGCACCTTTTGAAGCGCTCTATTTGGTCTCTCTGATTCAGCTGGGTATTAACT 421  
QY 430 TCGATCCAAAGCATTTGTTTGGCGTT 456  
Db 422 GCGATCCAAAGCATTTGTTTGGCGTT 448

RESULT 15  
BE919556 488 bp mRNA linear EST 02-OCT-2000  
LOCUS EST423325 potato leaves and petioles Solanum tuberosum cDNA clone  
DEFINITION cSTB1D22 5' sequence, mRNA sequence.  
ACCESSION BE919556  
VERSION BE919556  
KEYWORDS EST  
SOURCE EST  
ORGANISM Solanum tuberosum  
REFERENCE 1 (bases 1 to 488)  
AUTHORS van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.  
TITLE Generation of ESTs from potato leaves and petioles  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone request: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com.

FEATURES  
source 1. .488  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db xref="taxon:4113"  
/clone="cSTB1D22"  
/clone\_lib="potato leaves and petioles"

/tissue\_type="leaflets and petioles"  
/dev\_stage="8 weeks old plants"  
/lab\_host="SOLR"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."

BASE COUNT 110 a 113 c 116 g 149 t  
ORIGIN

Query Match 40.8%; Score 422; DB 12; Length 488;  
Best Local Similarity 94.1%; Pred. No. 1.7e-97;  
Matches 450; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 6 AACATACATTGCTACGTTACAGATAAATATCTTGTCTCATTTTCAGTTCCAAAACCTG 65  
Db 14 AAGCAAAACATTGTTAGCTTTACAGATAAATAGCCTGTGCTCGTTTCAGTTCCAAAACCTG 72  
QY 66 AAGAAGAGAGAGAGACAATGGAAGTTTCAACATCGTTCTTCGACTCGCAATCTGCC 125  
Db 73 --GAAGAAGAGAGAGAGATATGGAAGTTTCAACATCGTTCTTCGACTCGCAATCTGCC 130  
QY 126 TCTCGCAACCGCTGGAGTTATGATTTCTCAAAAACCTTCGCGCAGATCTCACTCTCGTT 185  
Db 131 TCTCGCAACCGCTGGAGTTATGATTTCTCAAGAAGTTTCGCGCAGATCTCACTCTCGTT 190  
QY 186 CAATCTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCT 245  
Db 191 CAATCTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCT 250  
QY 246 GGGGCTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGTTCATG 305  
Db 251 GGAGCTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGTTCATG 310  
QY 306 GGAGCATGCTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTT 365  
Db 311 GGAGCATGCTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTT 370  
QY 366 CTGATGGCAGCTGCATTTTGAAGCGCTCTATTTGGTCTCTCTGATTCAGCTGGGCATT 425  
Db 371 CTGATGGCAGCTGCATTTTGAAGCGCTTCTATTGGTCTCTCTGATTCAGCTGGGCATT 430  
QY 426 AACTTCGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTTGTGCTGTTTGTGTT 483  
Db 431 AACTTCGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTTGTGCTGTTTGTGTT 488

Search completed: May 25, 2003, 11:25:15  
Job time : 1494 secs

GenCore version 5.1.5  
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OM protein - protein search, using sw model

Run on: May 25, 2003, 11:25:24 ; Search time 62 Seconds  
(without alignments)  
533.002 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272  
Sequence: 1 MEGFTSFDDQSASNRWSY.....LIIMLNASEKKBKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688.5	54.1	213	22	Testis Enhanced Ge
2	499.5	39.3	140	22	Testis Enhanced Ge
3	498.5	39.2	138	21	Arabidopsis thalia
4	498.5	39.2	154	21	Arabidopsis thalia
5	495	38.9	110	21	Arabidopsis thalia
6	492.5	38.7	129	21	Arabidopsis thalia
7	491.5	38.6	236	22	Bovine mammary tis
8	483.5	38.0	255	21	Lung cancer assoc
9	477.5	37.5	237	19	Bax inhibitor BI-1
10	331.5	26.1	245	23	Human ovarian anti

11	324	25.5	277	22	AAU30218	Novel human secret
12	312	24.5	245	22	ABE63069	Drosophila melanog
13	192	15.1	305	22	AB357985	Drosophila melanog
14	172	13.5	341	22	AB358798	Drosophila melanog
15	171	13.4	346	21	AAS49311	Mouse brown adipos
16	166	13.1	122	21	AAG03753	Human secreted pro
17	165	13.0	242	22	AB644490	Human secreted pro
18	165	13.0	345	20	AAW81998	Human adult testis
19	165	13.0	345	21	AAV79139	Human haemopoietic
20	165	13.0	345	21	AAV66631	Membrane-bound pro
21	165	13.0	345	21	AAV59435	Human DERP2 protei
22	165	13.0	345	22	AAV65154	Human PRO281 (UNO2
23	165	13.0	345	23	ABP61812	Human polypeptide
24	165	13.0	345	23	ABG34030	Human Pro peptide
25	165	13.0	345	23	ABB89838	Human polypeptide
26	165	13.0	346	19	AAW74901	Human secreted pro
27	165	13.0	351	20	AAV76620	Human ovarian tumo
28	165	13.0	351	21	AAAB43975	Human cancer assoc
29	143.5	11.3	250	22	AAAB4489	Gene 16 human secr
30	132	10.4	319	21	AAV33283	Human TPAAAG12 pol
31	128.5	10.1	241	20	AAV37315	Protein which is s
32	123	9.7	290	21	AAV33365	Zea mays protein f
33	123	9.7	324	22	ABE60180	Drosophila melanog
34	118.5	9.3	221	21	AAV33367	Zea mays protein f
35	118.5	9.3	239	22	ABE60197	Drosophila melanog
36	118.5	9.3	243	21	AAV33366	Zea mays protein f
37	112.5	8.8	222	21	AAV44724	Zea mays protein f
38	112.5	8.8	238	20	AAV59658	Secreted protein f
39	112.5	8.8	250	21	AAV44723	Zea mays protein f
40	112	8.8	230	21	AAV52201	Arabidopsis thalia
41	112	8.8	245	21	AAV52200	Arabidopsis thalia
42	112	8.8	256	21	AAV52199	Arabidopsis thalia
43	111	8.7	238	21	AAV77122	Human neurotransm
44	111	8.7	238	22	AAV93503	Human polypeptide
45	111	8.7	293	21	AAV42202	Human ORFX ORF1966

#### ALIGNMENTS

RESULT 1  
AA65755  
ID AAB65755 standard; Protein; 213 AA.  
XX AAB65755;  
AC  
XX 27-MAR-2001 (first entry)  
DT  
XX Testis Enhanced Gene Transcript protein #1.  
DE  
XX Cell death modulator; programmed cell death; PCD; apoptosis;  
KW forestry plant.  
XX  
XX Pinus radiata.  
XX  
XX WO200075331-A1.  
XX  
XX 14-DEC-2000.  
XX  
XX 02-JUN-2000; 2000WO-NZ00086.  
XX  
XX 04-JUN-1999; 99US-0325932.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX Flinn B, Lasham A;  
XX  
XX WPI; 2001-061724/07.  
XX N-PSDB; AAF4782.  
XX  
XX Novel defender against cell death polynucleotide useful for modulating  
XX programmed cell death pathway and specific development pathways in  
XX

PT forestry plant -  
 XX Claim 22; Pages 81-82; 142pp; English.  
 PS  
 XX The present invention relates to coding sequences (see AAP44740-F44840  
 CC and AAP44843-F44844) and proteins (see AAB65714-B65814) involved in  
 CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
 CC of the present invention are useful for modulating a PCD or cell death  
 CC pathway and various developmental pathways in a forestry plant, by  
 CC stably incorporating one of the present coding sequences into the genome  
 CC of the forestry plant, where the coding sequence provides a PCD pathway  
 CC that is not present in a native form of the forestry plant.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 54.1%; Score 688.5; DB 22; Length 213;  
 Best Local Similarity 64.6%; Pred. No. 3.8e-73;  
 Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;  
 OY 39 QVYLTCCALVASAGAYHILWNIIGLLTTMACGSMVWLLSAP--PYQOKRVALIMA 96  
 DB 1 RYVLSLSCALVTAAGVYHLLNLNIGLLTGLACIGSVIGLLSVPTSSNNGKRAALLA 60  
 OY 97 AALFEGASGPIELGINDPDSIVFGAFVGCVAVFCFSAAAMLARREYLYLGGLLSSG 156  
 DB 61 AAFKATGATGLIDAVINIDSSILVSFAFGTSLAFACFSAAAITARREYLYLGGLLSG 120  
 OY 157 VSLFWLHFASSIFGGSMAVFKFELYFGLLVFGVIVFDQTEIIEKALHGMVDYVKHALT 216  
 DB 121 ISTIMWLQASSIFGGSAAIYFETIYFGLLVFLGYIIFDTQMIIEKADHGDYDYKXSLD 180  
 OY 217 LFTDFGAVFVRILIIIMKNA-SEKSEKKKKRR 247  
 DB 181 LFTDFVAVFVRLVIMAKNADSKREGKKRR 212  
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 ID AAB65756 standard; Protein; 140 AA.  
 AC AAB65756;  
 DT 27-MAR-2001 (first entry)  
 XX Testis Enhanced Gene Transcript protein #2.  
 DE Cell death modulator; programmed cell death; PCD; apoptosis;  
 XX forestry plant.  
 KW Pinus radiata.  
 XX WO200075331-A1.  
 XX 14-DEC-2000.  
 XX 02-JUN-2000; 2000WO-NZ00086.  
 XX 04-JUN-1999; 99US-0325932.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX Flinn B, Lasham A;  
 XX WPI; 2001-061724/07.  
 DR N-PSDB; AAF44783.  
 XX Novel defender against cell death polynucleotide useful for modulating  
 PT programmed cell death pathway and specific development pathways in  
 PT forestry plant -  
 XX Claim 22; Page 82; 142pp; English.  
 PS  
 CC The present invention relates to coding sequences (see AAP44740-F44840  
 CC and AAP44843-F44844) and proteins (see AAB65714-B65814) involved in  
 CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
 CC of the present invention are useful for modulating a PCD or cell death  
 CC pathway and various developmental pathways in a forestry plant, by  
 CC stably incorporating one of the present coding sequences into the genome  
 CC of the forestry plant, where the coding sequence provides a PCD pathway  
 CC that is not present in a native form of the forestry plant.  
 XX  
 SQ Sequence 140 AA;  
 Query Match 39.3%; Score 499.5; DB 22; Length 140;  
 Best Local Similarity 66.2%; Pred. No. 5.8e-51;  
 Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;  
 OY 1 MEGTSPFDSOSASRNWSDSLKNFRQISPLVOTHLKQVYLTCCALVASAGAYHIL 60  
 DB 1 MDAFASLFQS---SGKGMHSDSLKNFRQISPAVQSHLKNYLSLCCALMASAGGAYLHLM 57  
 OY 61 WNIGGLTTMACGSMVWLLSAPPYQOKRVALIMAALFEGASIGLIELGINFDPDSIV 120  
 DB 58 LNIGGLTTIACISIVWLLSIPPHSEQKFGLLMAALFEGACIGLIEALIKVDPSIV 117  
 OY 121 FOAFVGCVAVFCFSAAAMLARREYLYLGG 151  
 DB 118 ISAFVGSALAPACFSGAA-----CWLGG 140  
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 AC AAG19970;  
 DT 17-OCT-2000 (first entry)  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 21975.  
 DE Arabidopsis thaliana  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 XX termination sequence.  
 OS Arabidopsis thaliana.  
 XX EP1033405-A2.  
 XX 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-0301439.  
 XX 25-FEB-1999; 99US-0121825.  
 XX 05-MAR-1999; 99US-0123180.  
 XX 09-MAR-1999; 99US-0123548.  
 XX 23-MAR-1999; 99US-0125788.  
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 XX 01-APR-1999; 99US-0127462.  
 XX 06-APR-1999; 99US-0128234.  
 XX 08-APR-1999; 99US-0128714.  
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Best local similarity 70.8%; Pred. No. 7.5e-51;
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RESULT 4
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ID AAG19969 standard; Protein; 154 AA.
XX
AC AAG19969;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21974.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159394.  
PR 13-OCT-1999; 99US-0159395.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.

PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 28-OCT-1999; 99US-0162142.  
PR 29-OCT-1999; 99US-0162142.  
Query Match 38.9%; Score 495; DB 21; Length 110;  
Best Local Similarity 86.4%; Pred. NO. 1.4e-50;  
Matches 95; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
QY 139 MLARREYVLGGILSSGVSLFLWHPASSIFGGSMAVFKFELYFGLLVFGVYVFDTQE 198  
Db 1 MLARREYVLGGILSSGVSLFLWHPASSIFGGSMAVFKFELYFGLLVFGVYVFDTQE 60  
QY 199 IIEKAHLGDMYVYKHALTFDFAVFEVRLIIMLNKNSADKEKKKKRN 248  
Db 61 IIEKAHLGDMYVYKHALTFDFAVFEVRLIIMLNKNSADKEKKKKRN 110  
RESULT 6  
AAG54829  
ID AAG54829 standard; Protein; 129 AA.  
XX AC AAG54829;  
XX DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 70059.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EPI033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0125788.  
XX PR 25-MAR-1999; 99US-0126264.  
XX PR 28-MAR-1999; 99US-0126785.  
XX PR 01-APR-1999; 99US-0127482.  
XX PR 06-APR-1999; 99US-0128234.  
XX PR 08-APR-1999; 99US-0128714.  
XX PR 16-APR-1999; 99US-0129845.  
XX PR 19-APR-1999; 99US-0130077.  
XX PR 21-APR-1999; 99US-0130449.  
XX PR 23-APR-1999; 99US-0130510.  
XX PR 23-APR-1999; 99US-0130891.  
XX PR 28-APR-1999; 99US-0131449.  
XX PR 30-APR-1999; 99US-0132048.  
XX PR 30-APR-1999; 99US-0132407.  
XX PR 04-MAY-1999; 99US-0132484.  
XX PR 05-MAY-1999; 99US-0132485.  
XX PR 06-MAY-1999; 99US-0132486.  
XX PR 06-MAY-1999; 99US-0132487.  
XX PR 07-MAY-1999; 99US-0132863.  
XX PR 11-MAY-1999; 99US-0134256.  
XX PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135623.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139817.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 03-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147360.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149388.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 23-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150586.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 30-AUG-1999; 99US-0151080.  
 PR 31-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155182.  
 PR 24-SEP-1999; 99US-0155486.  
 PR 28-SEP-1999; 99US-0155659.  
 PR 29-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159337.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 18-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 22-OCT-1999; 99US-0160989.

PR 25-OCT-1999; 99US-0161404.  
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 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 38.7%; Score 492.5; DB 21; Length 129;  
 Best Local Similarity 71.4%; Pred. NO. 3.5e-50;  
 Matches 90; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 1 MEGTGFDFDSQASRNRSYDLSLKNPQISPLVQTHLKQVYLTCCALVASAAGAYLHIL 60  
 DB 1 MDAESFFDSQPGSRS-WSYDLSLKNPQISPAVQNHKXVYLTCCALVASAAGAYLHVL 59  
 QY 61 WNTGGLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINDPSIV 120  
 DB 60 WNTGGLTTTTCIGTMTLLSCPPYEHQRLSLFASAVLEGASVGLIKVAIDVDPISIL 119  
 QY 121 FGATVG 126  
 DB 120 ITATVG 125

RESULT 7  
 AAB87615  
 ID AAB87615 standard; protein; 236 AA.  
 XX AAB87615;  
 AC AAB87615;  
 XX AAB87615;  
 DT 15-MAY-2001 (first entry)  
 DE Bovine mammary tissue derived protein #6.  
 XX Bovine; mammary gland; cancer; tumour; angiogenesis.  
 KW Bos taurus.  
 OS Bos taurus.  
 XX WO200114553-A1.  
 PN WO200114553-A1.  
 XX 01-MAR-2001.  
 PD 23-AUG-2000; 2000WO-NZ00166.  
 PR 23-AUG-1999; 99US-0150330.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
 XX Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;  
 DR WPI; 2001-226619/23.  
 XX New polypeptides and polynucleotides encoding the polypeptides, which  
 PT are expressed in bovine mammary gland tissue, useful for stimulating  
 PT mammary gland growth or function, or inducing differentiation of milk  
 PT producing cells -  
 XX Claim 11; Page 62; 97pp; English.  
 BS The present invention relates to proteins derived from bovine  
 XX mammary gland cells. The invention is useful for stimulating  
 CC bovine mammary gland cell growth and function, inhibiting the  
 CC growth of various mammary gland cancer cells, inhibiting  
 CC angiogenesis and vascularization of tumours, or modulating  
 CC the growth of blood vessels in a mammal.  
 XX Sequence 236 AA;  
 SQ

Query Match 38.6%; Score 491.5; DB 22; Length 236;  
Best Local Similarity 42.9%; Pred. No. 1e-49;  
Matches 99; Conservative 53; Mismatches 72; Indels 7; Gaps 4;

QY 19 SYDSLKNFROISPLVQTHLKVYTLCCALVASAAGAYLHILWNI--GGLLTTMACGSM 76  
Db 9 NFDALFRPSHITSTQOHLKKVYASALCMFVAAGAYIHVVTHFTQAGLLSALGSLGM 68  
QY 77 VWLTSAPPYQ--EQKRVALLMAALFEGASIGLPIELGINFDPFSIVFGACVAVFCF 134  
Db 69 IWLWATPHSHETEQRKGLLAGFAFLTGVGLPALDLCIAINPSILPTAFMGTAIPTCF 128  
QY 135 SAAMLAARREYLYLGLSSGVSLFLWLFHFASSIFGSGMAYFKPELYGLAVFVGYIVE 194  
Db 129 TLSALYARRRSYFLGGLILMSALMLD--LSSLGNLFEGSVVLFQANLYMGLVVMCGFVLF 187  
QY 195 DTQRIIEKAHLGDMYVYKHALTFTDFGAVFVRILIMLKNASEKEEKKK 245  
Db 188 DTQLIIEKAENGDKYIWHCVDFLDFVTLFRKLMILAWN--EKDKKKK 236

RESULT 8  
AAB58178  
ID AAB58178 standard; Protein; 255 AA.  
XX AC AAB58178;  
XX DT 14-MAR-2001 (first entry)  
XX DE Lung cancer associated polypeptide sequence SEQ ID 516.  
XX KW Human; lung cancer associated protein; neuroprotective; cytostatic;  
XX KW cardioactive; immunomodulatory; muscular active; vulnerary;  
XX KW gastrointestinal; nephrotropic; antiinfective; gynecological;  
XX KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
XX KW proliferative disorder; wound healing; infectious disease.  
XX OS Homo sapiens.  
XX PN W0200055180-A2.  
XX PD 21-SEP-2000.  
XX PF 08-MAR-2000; 2000WO-US05918.  
XX PR 12-MAR-1999; 99US-0124270.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (ROSE/) ROSEN C.A.  
XX FI Ruben SM;  
XX DR WPI; 2000-587514/55.  
XX DR N-PSDB; AAF18054.  
XX PT Lung cancer associated gene sequences, referred to as lung cancer  
XX PT antigens, useful for treatment, prevention, and diagnosis of disorders  
XX PT such as lung cancer -  
XX PS Claim 11; Page 1006-1007; 1425pp; English.  
XX CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer  
XX CC associated proteins represented in AAB58106 - AAB58548. Lung cancer  
XX CC associated proteins and polynucleotide sequences, their agonists, and  
XX CC antagonists may have neuroprotective; cytostatic; cardioactive;  
XX CC immunomodulatory; muscular active general; vulnerary; gastrointestinal  
XX CC general; nephrotropic; antiinfective; gynecological; or antibacterial  
XX CC activity. The invention also includes antibodies specific for the  
XX CC protein or polynucleotide sequences. The lung cancer associated  
XX CC polynucleotide sequences may be used for detection of lung cancer,  
XX CC chromosome identification, as chromosome markers, and for numerous other  
XX CC diagnostic or research purposes. The proteins may be used to treat  
XX CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders. The proteins may also be used in the treatment of wounds and  
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
CC peptide AAB58549 are used in the course of the invention for the  
CC identification and characterisation of the polynucleotide and protein  
CC sequences.  
XX SQ Sequence 255 AA;  
Query Match 38.0%; Score 483.5; DB 21; Length 255;  
Best Local Similarity 41.1%; Pred. No. 1e-48;  
Matches 102; Conservative 54; Mismatches 79; Indels 13; Gaps 5;

QY 3 GFTSFDSQASSENKWSYDLSKNFQISPLVQTHLKVYTLCCALVASAAGAYLHILWN 62  
Db 17 GTWNIIFD-----RKINFDALKFKSHIPTSTQOHLKKVYASALCMFVAAGAYHVMYTH 70  
QY 63 I--GGLLTTMACGSMVWLLSAPPYQ--EQKRVALLMAALFEGASIGLPIELGINFDPFS 118  
Db 71 FIQAGLLSALGSLILIMLWATPHSHETEQRKGLLAGFAFLTGVGLPALDLCIAINPS 130  
QY 119 IVFGAFVGCNAVVEGCSAAAMLARREYLYLGLSSGVSLFLWLFHFASSIFGSGMAYFK 178  
Db 131 ILPTAFMGTAIPTCFITLSALYARRRSYFLGGLILMSALSL--LSSLGNVFFGSIWLFQ 189  
QY 179 FELYGLLVFVGIVYVDTQRIIEKAHLGDMYVYKHALTFTDFGAVFVRILIMLKNASE 238  
Db 190 ANLYVGLVVMCGFVLFDTQLIIEKAENGDDYIWHCIDLDFLDFITVFRKLMILAWN--E 247  
QY 239 KEKKKKK 246  
Db 248 KDKKKKK 255

RESULT 9  
AAW73136  
ID AAW73136 standard; Protein; 237 AA.  
XX AC AAW73136;  
XX DT 02-FEB-1999 (first entry)  
XX DE Bax inhibitor BI-1.  
XX KW Bax inhibitor; BI-1; human; apoptosis.  
XX OS Homo sapiens.  
XX PH Location/Qualifiers  
XX FT 30..50  
XX FT Domain /note= "transmembrane domain"  
XX FT 55..73  
XX FT Domain /note= "transmembrane domain"  
XX FT 85..103  
XX FT Domain /note= "transmembrane domain"  
XX FT 117..135  
XX FT Domain /note= "transmembrane domain"  
XX FT 141..160  
XX FT Domain /note= "transmembrane domain"  
XX FT 162..187  
XX FT Domain /note= "transmembrane domain"  
XX PN W09840397-A1.  
XX PD 17-SEP-1998.  
XX PF 13-MAR-1998; 98WO-US05015.  
XX PR 14-MAR-1997; 97US-0818514.  
XX PA (BURN-) BURNHAM INST.  
XX FI Reed JC, Xu Q;

XX WPI; 1998-531519/45.  
DR N-PSDB; AAV59067.  
XX  
PT Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate  
PT cellular apoptotic activity or identify agents altering BI-1 or BI-2  
PT binding which can modulate apoptotic activity  
XX  
PS Claim 14; Fig 1; 80pp; English.  
XX  
XX This is the amino acid sequence of an inhibitor protein, termed  
CC BI-1, of the pro-apoptotic protein Bax. Nucleic acids encoding  
CC BI-1 (see AAV59067) and BI-2 (see AAV59068) were identified by  
CC suppression of Bax-induced death of yeast cells transformed to  
CC express human Bax. A human HepG2 cDNA library was used for library  
CC screening. The invention provides vectors, optionally expression  
CC or viral vectors, containing BI nucleic acids, and host cells  
CC containing these vectors.  
CC be used to increase expression of these proteins in cells, or  
CC antisense molecules prepared from them used to decrease expression.  
CC In these ways, cellular apoptotic activity may be modulated. The  
CC Bis and peptide portions are useful to detect, e.g. another BI or a  
CC member of the Bcl-2 family in biological samples. They are  
CC especially useful in assays to identify agents (e.g. organic  
CC molecules or peptides; claimed) modulating the specific association  
CC of BI-1/BI-2 with a second protein (e.g. a BI, an anti-BI antibody  
CC or a Bcl-2 family protein (e.g. Bax) (Claimed)) e.g. in screening  
CC for drugs to treat pathologies characterised by aberrant apoptotic  
CC activity. The agents can then be contacted with cells to modulate  
CC cellular apoptotic activity (claimed). Bax overexpression is  
CC associated with e.g. neuronal cell death due to ischaemia, epilepsy,  
CC spinal cord injury, Parkinson's disease and Alzheimer's disease.  
CC Antibodies raised against the Bis and peptides are also useful e.g.  
CC to detect/quantify Bis in biological samples.  
XX  
SQ Sequence 237 AA;  
XX  
Query Match 37.5%; Score 477.5; DB 19; Length 237;  
Best Local Similarity 42.2%; Pred No. 4.8e-48;  
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;  
QY 19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAGAYHLHLMNI--GGLTTMACWGM 76  
DB 9 NFDALLKFHSHTPTQHLKQVYASFPALCMFVAARAGAYVHMVTHFIQAGLLSALGSLIM 68  
QY 77 VWLLSAPPVQ--EOKRVALLMAALFEFSGISGLTELGINFDPSVFCGAVGCAVFGCF 134  
DB 69 IWLMPHSHETEQKXGLGLLAFGLTGLGPALEFCIAVNFSLPFAFGTAVITCF 128  
QY 135 SAAMLARREYLYLGLLSSGYSLLFWLHFASSIFGSMVAFKFLYFGLLVFGYIVF 194  
DB 129 TSLGALYARRRSYLFLOGILMSALSILL--LSSLGNVFFGSIWLFQANLYGLVWCGFVLF 187  
QY 195 DTQETIEKAHLGMDYVKAHLTFDFAVAVFVRIILMLKNASEKKEKKR 246  
DB 188 DTQLIIEKAEBGQDYVHCIDFLDFITVFRKLMILANN--EKDKKKKK 237  
RESULT 10  
ID ABP42996  
XX ABP42996 standard; Protein; 245 AA.  
XX  
AC ABP42996;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
XX Human ovarian antigen HPDWT56, SEQ ID NO:4128.  
XX  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW

cardiovascular disorder; respiratory disorder; neurological disorder;  
gastrointestinal disorder; urinary system disorder; drug screening;  
gene therapy; chromosome mapping; forensic analysis;  
antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
antiinflammatory; gynaecological; reproductive.  
Homo sapiens.  
WO200200677-A1.  
XX  
XX 03-JAN-2002.  
XX  
XX 07-JUN-2001; 2001WO-US18569.  
XX  
XX 07-JUN-2000; 2000US-209467P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
XX  
XX WPI; 2002-147878/19.  
XX  
XX N-PSDB; ABQ56073.  
XX  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
XX useful in the prevention, treatment and diagnosis of cancer (e.g.  
XX ovarian cancer), immune disorders, cardiovascular disorders and  
XX neurological diseases -  
XX  
XX Claim 11; SEQ ID No 4128; 2922pp; English.  
XX  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
XX to the sequences of the invention. The invention additionally relates to  
XX recombinant vectors and host cells comprising human ovarian antigen  
XX polynucleotides, antibodies against human ovarian antigens, and the use  
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
XX treating, prognosing or preventing various ovary and/or breast-related  
XX disorders. Such conditions include ovarian cancer and breast cancer, and  
XX metastatic tumours of ovarian or breast origin, reproductive system  
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,  
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
XX vaginitis), immune disorders (e.g., congenital and acquired  
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,  
XX respiratory disorders, neurological disorders, gastrointestinal disorders  
XX and urinary system disorders. Ovarian antigen polypeptides and  
XX polynucleotides may also be used in screening for compounds which  
XX modulate ovarian antigen expression or activity. The polynucleotides may  
XX further be used for gene therapy, chromosome mapping, in the  
XX identification of individuals and in forensic analysis, and the  
XX polypeptides may be used as food additives or to prepare antibodies  
XX useful in disease diagnosis, drug targeting and phenotyping. The present  
XX sequence represents a human ovarian antigen of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 245 AA;  
XX  
Query Match 26.1%; Score 331.5; DB 23; Length 245;  
Best Local Similarity 34.8%; Pred No. 1.1e-30;  
Matches 72; Conservative 46; Mismatches 78; Indels 11; Gaps 4;  
QY 3 GFTSFDDQSASRNWSYDLSKNFRQISPLVQTHLKQVYLTLCCALVASAGAYHLHLMNI 62  
DB 17 GTWNIFD-----RKINFALLKFHSHTPTQHLKQVYASFPALCMFVAARAGAYVHMVTH 70  
QY 63 I--GGLTTMACWGMVLLSAPPVQ--EOKRVALLMAALFEFSGISGLTELGINFDPS 118  
DB 71 FIOAGLLSALGSLIMVLMVTHPHSHETEQKXGLGLLAFGLTGLGPALEFCIAVNFSL 130



QY 119 IVEGAFVGCVAVFCGSAAMLARREYVYLVGLLSSGVSLLPWLFWLHFASSIFGGSMVAFK 178  
Db 131 ILPFAWGTAMIFCTLSALYARRSYLVFLGGLMSSPELGAFASLNGFPF-GSIWLFQ 189  
QY 179 FELYGLLVFVGVIYVFTQBIIEKAHL 205  
Db 190 ANLYXGLVVMCGFAFLIILNSLLKRPNM 216

RESULT 11  
AAU30218  
ID AAU30218 standard; Protein; 277 AA.  
XX AAU30218;  
AC  
DT 18-DEC-2001 (first entry)  
XX  
DE Novel human secreted protein #709.  
XX  
KW Human; vaccination; gene therapy; nutritional supplement;  
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
XX  
OS Homo sapiens.  
XX  
FN WO200179449-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 16-APR-2001; 2001WO-US08656.  
XX  
PR 18-APR-2000; 2000US-0552929.  
PR 26-JAN-2001; 2001US-0770160.  
XX  
FA (HYSE-) HYSEQ INC.  
XX  
PI Tang VT, Liu C, Drmanac RT;  
PI WPI; 2001-611725/70.  
DR  
XX Nucleic acids encoding a range of human polypeptides, useful in genetic  
PT vaccination, testing and therapy -  
XX  
PS Claim 20; Page 262; 765pp; English.  
XX  
CC The invention relates to novel human secreted polypeptides. The  
CC polypeptides and antibodies to the polypeptides are useful for  
CC determining the presence of or predisposition to a disease associated  
CC with altered levels of polypeptide. The polypeptides are also useful for  
CC identifying agents (agonists and antagonists) that bind to them. Cells  
CC expressing the proteins are useful for identifying a therapeutic agent  
CC for use in treatment of a pathology related to aberrant expression or  
CC physiological interactions of the polypeptide. Vectors comprising  
CC the nucleic acids encoding the polypeptides and cells genetically  
CC engineered to express them are also useful for producing the proteins.  
CC The proteins are useful in genetic vaccination, testing and  
CC therapy, and can be used as nutritional supplements. They may be used to  
CC increase stem cell proliferation; to regulate haematopoiesis; and in  
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
CC immune suppression and/or stimulation; as anti-inflammatory agents; and  
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
CC sequences of novel human secreted proteins of the invention.  
XX  
SQ Sequence 277 AA;  
Query Match 25.5%; Score 324; DB 22; Length 277;  
Best Local Similarity 35.0%; Pred. No. 9.8e-30;  
Matches 93; Conservative 51; Mismatches 88; Indels 34; Gaps 13;

QY 3 GTSFPDSASRNRWSYDLSKNFQISPLV-QTHLKVYITLCCALVSAAGAYLHLH 61  
Db 17 GTWNIPD-----RKITFDALLKFSHTFSTQQAHRMKKVYASFALCYFGAAGAYVNMVT 70

QY 62 NI--GGILTTMACMGSMWLLSAPPYQ--EOKRV--ALIMAAALFEGASIGPLI---ELG 112  
Db 71 HFTQAGLLSALGSLILMIWLMATPHSHETEQLGTSLGFCIPYRKLGLGALGSFVIA 130  
QY 113 INFDPISIVFOAFVCGA-VVFGCFSAAMLAARR-REYLYLGLLSSGVSLI-FWLHFASSI 169  
Db 131 VKRQASLP-TAFMGHSGNSFPAPFTLSALLCRPSYLFUGGILMSALSIVAFCLPLGNVF 189  
QY 170 FGGSMVAFKPELYGLLVFVGVIYVFTQBIIEKAHLGDMDY-VKHALTLFTDFGAVFVRI 228  
Db 190 FWIPFVVFQANLYVGLVVMCGFVLFDTQLIIEKABQGDQDYNLWHCIDLFLDFITVF--- 246  
QY 229 LIIMLVNASE-----KEKKKKRRN 248  
Db 247 ----QKNSMKDPGPFMKKDKKKRRN 268

RESULT 12  
ABB63069  
ID ABB63069 standard; Protein; 245 AA.  
XX ABB63069;  
AC  
XX 26-MAR-2002 (first entry)  
DT  
XX Drosophila melanogaster polypeptide SEQ ID NO 15999.  
DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
FN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
FA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
PI WPI; 2001-656860/75.  
DR N-PSDB; ABL07172.  
DR  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 15999; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABE57737-ABE72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 245 AA;

Query Match 24.5%; Score 312; DB 22; Length 245;  
Best Local Similarity 34.4%; Pred. No. 2.2e-28;  
Matches 77; Conservative 48; Mismatches 83; Indels 16; Gaps 5;

QY 31 PLVOTHLKQVYLTCCALVASAAGAYLHI--LWNIGLLTTTACMGSMWLLSAPPYQEQ 88  
 Db 25 PVREHLKSVYMWLSTAAATANGMLQMRDFLDG-----VLAAYVILVLVGLHFXKD 80  
 QY 89 -----KRVALLMAALFPGASIGPLIEIGINFDPSIVFGAFVGCVAVFGCFSAAMLARR 143  
 Db 81 GKNYVTRGLMAYAFGCGQTGLPGLGYICINPAIILSALTGTFTVTSLSLSALLAEQ 140  
 QY 144 RYVLYGLLSSGVSLFWLHPASSIFGSMVAFKFLYFGLLVFVGYIVFDTOEIEKA 203  
 Db 141 GXYLILGGLMWSVINTMALLSLFNWVF-KSYFVQVTQYVGVFWMAAFIVYDTONIVEKC 199  
 QY 204 HIGDMYVKHALTFTDFGCAVFRILIMLNASEKEKKKRR 247  
 Db 200 RGNREVDVQHLDLFFDVLSNFRLLIIL-----TKBERKQNER 239

RESULT 13  
 ABB57985  
 ID ABB57985 standard; Protein; 305 AA.  
 AC ABB57985;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 747.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL02088.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 747; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB161176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 15.1%; Score 192; DB 22; Length 305;  
 Best Local Similarity 25.7%; Pred No 5, 2e-14;  
 Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;

QY 36 HLKQVYLTCCALVASAAGAY-----LHILWNIIGLLTTTACM-----GSMVLLSAPPYQEQKRVALL 84

Db 85 HATYAFGASGVYTAASAVAFQSDAMMALMTRSGWVASLVTGLVMSGSIAQGLEYP 144  
 QY 85 YQEKRVALLMAALFPGASIGPLIEIGINFDPSIVFGAFVGCVAVFGCFSAAMLARR 144  
 Db 145 GFQAKQLAWLVHCAVL-GAVLAPWCLLG-----GPILTKALLYTSIGVIGALSTVACAPSE 199  
 QY 145 EYLYLGLLSSGVSLF-----WLHFASSIFGSMVAFKFLYFGLLVFVGYIVFDTO 197  
 Db 200 KFLHWGGLAIGLVGVFASSLASMWLPPTTAVGAG--LASMSLYGLLIFSGFLLYDTQ 256  
 QY 198 EIEKAHLGDM-----DYVKHALTFTDFGCAVFRILIMLNASEKEKKKRRN 248  
 Db 257 RIVKSAELYPQYSKFPYDPINHALAYMDALNIFRIAILAGD-----QKRKN 305

RESULT 14  
 ABB5798  
 ID ABB5798 standard; Protein; 341 AA.  
 AC ABB5798;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 3186.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL02901.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 3186; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB161176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 341 AA;  
 Query Match 13.5%; Score 172; DB 22; Length 341;  
 Best Local Similarity 26.5%; Pred No 1, 4e-11;  
 Matches 56; Conservative 46; Mismatches 77; Indels 32; Gaps 9;

QY 46 CALVASAAGAYL--HILWNI--GGLLTTTACM-----GSMVLLSAPPYQEQKRVALL 94

Search completed: May 25, 2003, 12:20:50  
Job time : 64 secs



```
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325.932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 88
LENGTH: 140
TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-88

Query Match
Best Local Similarity 39.3%; Score 499.5; DB 4; Length 140;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGFTSFDSASRRWSYSLKNFRQISPLVOTHLKQVYLTCCALVSAAGAYLHL 60
DB 1 MDAFASLFQS---SGKWSHSDSLNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHL 57
QY 61 WNIIGLLITTMACGSMYLLSAPPYQVQKRVALLMAALFEGASIGLIELGINFDPSTV 120
DB 58 LNIIGLLITTIACISIVWLLSIPHEQKRGFLMLMAALFEGACIGLIELAAIKVDPSIV 117
QY 121 FGAFVGCNVFGCPSAAMLARREYLYLGG 151
DB 118 ISAFVGSALAFCSGAA-----CWLG 140

RESULT 3
US-08-818-514-3
; Sequence 3, Application US/08818514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-818-514-3

Query Match
Best Local Similarity 37.5%; Score 477.5; DB 2; Length 237;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVOTHLKQVYLTCCALVSAAGAYLHLNII--GGLLITTMACGSM 76
DB 9 NFDALLKFSHITPSTQOHLKKVYSPALCNFVAAGAYVHMVTHFIOAGLLSALGSLIIM 68
QY 77 VMLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPSTVIFGAFVGCNVFGCF 134
DB 69 IWMATPHSHETEOKKLGLAGFAFLTGIGLGPALFECIAVNPISILPTAFMGTAIFTCF 128
QY 135 SAAAMLARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 194
DB 129 TISALYARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 187

Query Match
Best Local Similarity 37.5%; Score 477.5; DB 4; Length 237;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVOTHLKQVYLTCCALVSAAGAYLHLNII--GGLLITTMACGSM 76
DB 9 NFDALLKFSHITPSTQOHLKKVYSPALCNFVAAGAYVHMVTHFIOAGLLSALGSLIIM 68
QY 77 VMLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPSTVIFGAFVGCNVFGCF 134
DB 69 IWMATPHSHETEOKKLGLAGFAFLTGIGLGPALFECIAVNPISILPTAFMGTAIFTCF 128
QY 135 SAAAMLARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 194
DB 129 TISALYARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 187

Query Match
Best Local Similarity 42.2%; Pred. No. 3.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVOTHLKQVYLTCCALVSAAGAYLHLNII--GGLLITTMACGSM 76
DB 9 NFDALLKFSHITPSTQOHLKKVYSPALCNFVAAGAYVHMVTHFIOAGLLSALGSLIIM 68
QY 77 VMLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPSTVIFGAFVGCNVFGCF 134
DB 69 IWMATPHSHETEOKKLGLAGFAFLTGIGLGPALFECIAVNPISILPTAFMGTAIFTCF 128
QY 135 SAAAMLARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 194
DB 129 TISALYARRRYLYLGLLSGVSLLFHLFASIFGGSMVAFKFLYFGLLVFGYIVF 187
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[illegible]

EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670

EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 13.0%; Score 165; DB 4; Length 346;  
Best Local Similarity 26.3%; Pred. No. 4.1e-11;  
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;

QY 36 HUKQVTLCCALVASAGAYLH--ILWNI---GGLLT---TWACMGSMVWLLSAPPYQE 87  
DB 125 HSTYMYLAGSISGLTALSALISRTFVLNFMNMGWSWTIGVTFAMVYGAGMLVRSIPYDQ 184  
QY 88 Q---KRVALLMAAALFEGASIGPLIEGINFDPISVFGAFVGCAGVFGCFSAAMLARR 144  
DB 185 SPGRKHLAWLLHSGVM-CAVVAPLTILG---GPLLIRAAVMTAGIV--GGLSTVAMCAPSE 239  
QY 145 EYVYLGGLLSSGVSLFWLHFASIFGSGM-----AVKPELYFGLLVFGYIVF 194  
DB 240 KFLNMGAPLGVGLGV---FVSSL--GSMFLPTTVAGATLYSVAMYGLVLFSPMLLY 293  
QY 195 DTQEIIEKARHLDGM-----DYVKHALTLFTDFGAFVFRILIIMLKNASEKE 240  
DB 294 DTQKVKRAEYSPYGVQKYPINSMLSIYMDTLNIFRVATMLATGNGKK 345

RESULT 7  
US-09-247-155-89  
Sequence 89, Application US/09247155A  
Patent No. 6312922  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclet, Aymeric  
APPLICANT: Bouguerelet, Lydie  
TITLE OF INVENTION: Complementary DNAs  
FILE REFERENCE: GENSET.021A  
CURRENT APPLICATION NUMBER: US/09/247,155A  
CURRENT FILING DATE: 1999-02-09  
EARLIER APPLICATION NUMBER: 60/074,121  
EARLIER FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: 60/081,563  
EARLIER FILING DATE: 1998-04-13  
EARLIER APPLICATION NUMBER: 60/096,116  
EARLIER FILING DATE: 1998-08-10  
EARLIER APPLICATION NUMBER: 60/099,273  
EARLIER FILING DATE: 1998-10-04





```
Query Match      8.4%; Score 107; DB 2; Length 369;
Best Local Similarity 20.8%; Pred. No. 0.0003;
Matches 57; Conservative 41; Mismatches 90; Indels 86; Gaps 11;

QY 2 EGTSTFDSQSASRNSVDSLKNFRQISPLVQTHLKQVYLTLCAL-----V 49
DB 134 EGPSPSYNDQFPATWDDKSIR-----QAFIRKVELVLTQLSVLTSTVSFTFV 184
QY 50 ASAG-----AY-----LHIL-----WNIGLLTTMACGSMWLLS 81
DB 185 AEVGFVRENWVYVYAVFFSLIVLSGCCDFRRKHPNVLVALSVLTASISVMVGM1- 243
QY 82 APYQOKRVALLMAALPEGASIGPLI-ELGINDPDSIVFGAFVGCFAVFGCSRAAML 140
DB 244 ASFYNT-----AVINAVGITAVCTVVFISMQTRDYFTSCMGVLLVSMVVLFI 300
QY 141 ARREVLVYLGILLSSGVSLFVLFHFASSIFGSMVFKFELYGLLVFGVYVFDQII 200
DB 301 IRNR-----ILEIVAS-----LGALLFTCFPLAVDTQLL 330
QY 201 --EKALHGMVYKHALTFTDFGAVFVILIM 232
DB 331 GNKQLSPPEEYFAALNLYTDIINFILYLTII 364

RESULT 10
US-09-372-422A-28
; Sequence 28, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; PRIOR FILING DATE: 1999-08-11
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-28

Query Match      7.6%; Score 96.5; DB 4; Length 257;
Best Local Similarity 24.1%; Pred. No. 0.0031;
Matches 40; Conservative 33; Mismatches 58; Indels 35; Gaps 7;

QY 32 LVQTHLKQV--YLTLCALVASAAGAVLHILWNIGLLTTMACGSMWLLSAPPYQOK 89
DB 99 LVRGHITKRALLYVAAQLASSACIL-LRYLSGGVWTPVHALGAGI-----RPNQGLV 152
QY 90 RVALMAAALF-----EGASIGPIELGINDPDSIVFGAFVGC-AVVGCFSA 137
DB 153 NEVILTFSLFVTVAMILDPSQVRTIGPLT-----GLVAGNSLAGGNFTGA 201
QY 138 AMLARRRYLVGLLSSGVSLFVLFHFASSIFGSMVFKFELY 183
DB 202 SMNPARS-----FGPAMATGVWTHWVYVIGLLGGSLAGVYBSLF 243

RESULT 11
US-09-372-422A-30
; Sequence 30, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
```

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; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-30

Query Match      7.5%; Score 95.5; DB 4; Length 249;
Best Local Similarity 25.3%; Pred. No. 0.0039;
Matches 38; Conservative 22; Mismatches 65; Indels 25; Gaps 5;

QY 42 LTLCCALVASAAGAVLHILWNIGLLTTMACGSMWLLSAPPYQOKRVALLMA----- 96
DB 102 LYIAAQLASSAACPL-LRWLTGGLATFVHALAEGVPLQGVVAEAVTFSLLFVIYATI 160
QY 97 ---AALFEGASIGPIELGINDPDSIVFGAFVGCFAVVGCFSAAMLARRRYLVGLL 153
DB 161 LDPRKLLPGA--GPLLT-----GLLVGANSVAGAALSGASMPARSF---GPAV 204
QY 154 SSGVSLFVLFHFASSIFGSMVFKFELY 183
DB 205 ASGVWTHWVYVWVGLAGGPLAVLYVECCF 234

RESULT 12
US-08-794-216-3
; Sequence 3, Application US/08794216
; Patent No. 5843716
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,216
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0196 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
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CLONE: 238267  
US-08-794-216-3

Query Match 7.4%; Score 94.5; DB 2; Length 516;  
Best Local Similarity 21.4%; Pred. No. 0.014;  
Matches 56; Conservative 48; Mismatches 95; Indels 63; Gaps 14;  
QY 2 EGFSPFDSQASRNRWSYDLSKNFRQISPLVQTHLKQVYLTLCAL-VASAAGAYLHL 60  
DB 111 EGPSPYDNDQPPSVNWD-----KSIR-----QAFIRKVFVLTQLSVLTVAITFFV 160  
QY 61 WNIGGL-----LTTMACGSMWMLLSAPPYQEQKRVALLMAALFEG 102  
DB 161 GEVKGFRANVWTVYVVAIFFISLIVSCCGDF-----RKHPNWLVALSILT- 209  
QY 103 ASIGPLIELGINF--DPSIVFGAFVGCFAVFCFSAAM-LARREYLYLGLLSSGVSL 159  
DB 161 GEVKGFRANVWTVYVVAIFFISLIVSCCGDF-----RKHPNWLVALSILT- 209  
QY 160 LFWLHFPASSIFGSGMAVF---KFELYF---GLLVFVGYIVFDTEII--EKAHLGDMY 210  
DB 267 LF-----IF-AILCIFIRNRILIEIVVASLGALLFTCFLAVDTQLLGNKQLSLSP 318  
QY 211 VKHALTLFTDFGAVFVRIIIM 232  
DB 319 VFAALNLYTDIINIFLYLTII 340

RESULT 13  
US-08-749-289-3  
Sequence 3, Application US/08749289  
Patent No. 595301  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Coleman, Roger  
TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/749,289  
FILING DATE: Filed Herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0160 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 516 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-749-289-3

Query Match 7.4%; Score 94.5; DB 2; Length 516;

Best Local Similarity 21.4%; Pred. No. 0.014;  
Matches 56; Conservative 48; Mismatches 95; Indels 63; Gaps 14;  
QY 2 EGFSPFDSQASRNRWSYDLSKNFRQISPLVQTHLKQVYLTLCAL-VASAAGAYLHL 60  
DB 111 EGPSPYDNDQPPSVNWD-----KSIR-----QAFIRKVFVLTQLSVLTVAITFFV 160  
QY 61 WNIGGL-----LTTMACGSMWMLLSAPPYQEQKRVALLMAALFEG 102  
DB 161 GEVKGFRANVWTVYVVAIFFISLIVSCCGDF-----RKHPNWLVALSILT- 209  
QY 103 ASIGPLIELGINF--DPSIVFGAFVGCFAVFCFSAAM-LARREYLYLGLLSSGVSL 159  
DB 210 ISLSYVWGMIASFYNTAEVIMAVGITTAV---CFTVVFISMOTRYDFTSCGVLLVSVVV 266  
QY 160 LFWLHFPASSIFGSGMAVF---KFELYF---GLLVFVGYIVFDTEII--EKAHLGDMY 210  
DB 267 LF-----IF-AILCIFIRNRILIEIVVASLGALLFTCFLAVDTQLLGNKQLSLSP 318  
QY 211 VKHALTLFTDFGAVFVRIIIM 232  
DB 319 VFAALNLYTDIINIFLYLTII 340

RESULT 14  
US-09-372-422A-26  
Sequence 26, Application US/09372422A  
Patent No. 6313375  
GENERAL INFORMATION:  
APPLICANT: Francois Barrieu  
APPLICANT: Rudolf Jung  
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof  
FILE REFERENCE: 0919  
CURRENT APPLICATION NUMBER: US/09/372,422A  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: US 60/098,692  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 272  
TYPE: PRT  
ORGANISM: Zea mays  
US-09-372-422A-26

Query Match 7.4%; Score 94; DB 4; Length 272;  
Best Local Similarity 22.6%; Pred. No. 0.0067;  
Matches 48; Conservative 32; Mismatches 70; Indels 62; Gaps 9;  
QY 32 LVQTHLKQVYLTLCOA---LVASAAGAYLHLNIGLTTMACGSMWMLLSAPPYQEQ 88  
DB 97 MYRGHITKLRVLYVAAQLLASSAACVLLRFL--SGMVTFFVHALGRGI-----SPMOGL 149  
QY 89 KEVALLMAALF-----EGASIGPLIELGINFDPISIVFGAFVGC-AVVFQCFSA 136  
DB 150 VNEVILTFSLFVYVAMILDPRSQVRAIGLLT-----GLIVGANSIAGNFTG 198  
QY 137 AAMLARREYLYLGLLSSGVSLFVWLHFASSIFGSGMAVKFELYPGLLVFVGYIVFD 196  
DB 199 ASMNPARS---FGPALATGDWTHNVVWVWIGPLLGGLAGFVYESLF-----241  
QY 197 QELIEKAHLGDMY-----VKEALTIF 218  
DB 242 ---LVOKMHEAAQMGSLTTISPCVVAHASCILF 271

RESULT 15  
US-07-879-617A-12  
Sequence 12, Application US/07879617A  
Patent No. 5580775  
GENERAL INFORMATION:  
APPLICANT: Fremieu Jr., Robert T.  
APPLICANT: Caron, Marc G.

APPLICANT: Blakely, Randy D.  
TITLE OF INVENTION: A High Affinity L-Proline Transporter  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,617A  
FILING DATE: 19920501  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: EMU109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 607 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rattus  
TISSUE TYPE: Brain - serotonin transporter  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 95..96  
OTHER INFORMATION: /note= "Leucine zipper motif"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 102..103  
OTHER INFORMATION: /note= "Leucine zipper motif"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 109..110  
OTHER INFORMATION: /note= "Leucine zipper motif"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 116..117  
OTHER INFORMATION: /note= "Leucine zipper motif"

US-07-879-617A-12  
Query Match 6.8%; Score 87; DB 1; Length 607;  
Best Local Similarity 22.7%; Pred. No. 0.14; Mismatches 64; Indels 94; Gaps 15;  
Matches 55; Conservative 29;

QY 16 NRWSYDSLKNP-----RQISPLVQTHLKV-----YLTICCAL 48  
DB 179 NSWNTGNTNYAQDNITWTLHSTSPAEFYLRHVLIHQSKGLQDLGTTISWQTLTLCIVL 238  
QY 49 VASAGAYLHILNIGGLTLMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPL 108  
DB 239 IFTV--IYFSI-WK-GVATIS---GKVWWTATFPY-----IVLSVLLVRGATL--- 279  
QY 109 IELGINFDPISIVFGAFVGCVAFFGCSAAMLARRELYYL-----GGLSSGVSLLEWHL 164  
DB 280 -----FGAWRG--VVF-----YLPKNWQKLEETGV-----WVD 305

QY 165 PASSIFGGSMAVFKPELYFG-LLVFGVGVIVDT---QELIEKAHLGDMVYVKHALTILFTD 220  
DB 306 AAAQIF-----FSLGPGFGVLLAPASINKFNNNCYQDALVTSVNNCMTSFVSGFVIFTV 359  
QY 221 FG 222  
DB 360 LG 361  
Search completed: May 25, 2003, 12:24:35  
Job time : 37 secs

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein research, using sw model

Run on: May 25, 2003, 12:22:59 ; Search time 54 Seconds  
(without alignments)  
455.460 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDQSASRNWSY.....LIIMLNKXASEKKEKKRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB\_PEP.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB\_PEP.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB\_PEP.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1272	100.0	248	9	US-09-955-526-4
2	988	77.7	244	9	US-10-167-015-16
3	963.5	75.7	247	9	US-10-219-220-274
4	955	75.1	261	9	US-10-167-015-18
5	884.5	69.5	252	9	US-10-167-015-32
6	878.5	69.1	258	9	US-10-167-015-34
7	878.5	69.1	285	9	US-10-167-015-6
8	853	67.1	252	9	US-10-167-015-4
9	786.5	61.8	250	9	US-10-167-015-2
10	772.5	60.7	255	9	US-10-219-220-273
11	688.5	54.1	213	9	US-10-219-220-87
12	499.5	39.3	140	9	US-10-219-220-88
13	484.5	38.1	141	9	US-10-167-015-8
14	483.5	38.0	255	10	US-09-925-302-516
15	339	26.7	78	9	US-10-167-015-20
16	165	13.0	345	9	US-09-992-598-2
17	165	13.0	345	9	US-09-989-735A-2
18	165	13.0	345	9	US-09-989-735-2
19	165	13.0	345	9	US-09-990-444-2

#### ALIGNMENTS

##### RESULT 1

US-09-955-526-4

; Sequence 4, Application US/09955526

; Publication No. US20030009785A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods

; FILE REFERENCE: P-LJ 4868

; CURRENT APPLICATION NUMBER: US/09/955,526

; PRIOR FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: US 09/661,014

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Lycopersicon esculentum

; US-09-955-526-4

Query Match 100.0%; Score 1272; DB 9; Length 248;

Best Local Similarity 100.0%; Pred. No. 5.4e-115;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGTSPFDQSASRNWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHIL 60

Db 1 MEGTSPFDQSASRNWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHIL 60

QY 61 WNIIGLLTTMACMSMWLLSAPPYQSKRVALLMAALPEGASIGPLIELGNFDPISIV 120

Db 61 WNIIGLLTTMACMSMWLLSAPPYQSKRVALLMAALPEGASIGPLIELGNFDPISIV 120

QY 121 FCAFVGCAVFGCFSAAMLARREYLYLGLLSSGVSLLFWLHFASSIFGGSMVAFKPE 180

Db 121 FCAFVGCAVFGCFSAAMLARREYLYLGLLSSGVSLLFWLHFASSIFGGSMVAFKPE 180

QY 181 LYFGLLVFGYIVFTQBIIEKAHLGMDYVVKHALTFTDFGAVFVRILLIMLNASEKE 240

Db 181 LYFGLLVFGYIVFTQBIIEKAHLGMDYVVKHALTFTDFGAVFVRILLIMLNASEKE 240

QY 241 EKKXKRN 248

Db 241 EKKKRRN 248  
|||||

## RESULT 2

US-10-167-015-16  
; Sequence 16, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Jchal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; FILE REFERENCE: 1388  
; CURRENT APPLICATION NUMBER: US/10/167,015  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,478  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-167-015-16

Query Match 77.7%; Score 988; DB 9; Length 244;  
Best Local Similarity 75.5%; Pred. No. 1.3e-87;  
Matches 185; Conservative 32; Mismatches 24; Indels 4; Gaps 1;  
  
QY 4 FTSPFDSQASRNWSVDSLKNFROISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 63  
Db 4 FNSFFD-----SRRNWYDTLKNFROISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 59  
  
QY 64 GGLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGINFDPISVFGA 123  
Db 60 GGLTTVACMGSSFWLLSTPPEERKRVALLMAALFEGASIGPLIELGINFDPISVFGA 119  
  
QY 124 FVGCNAVFCFSAAMARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 183  
Db 120 FVGPALAFACFSAALVARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 179  
  
QY 184 GLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKKE 243  
Db 180 GLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKKE 239  
  
QY 244 KRRN 248  
Db 240 KRRD 244  
|||||

## RESULT 3

US-10-219-220-274  
; Sequence 274, Application US/10219220  
; Publication No. US20030082724A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of plant development  
; FILE REFERENCE: 11600.1022a1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 274  
; LENGTH: 247  
; TYPE: PRT

; ORGANISM: Eucalyptus grandis  
US-10-219-220-274

Query Match 75.7%; Score 963.5; DB 9; Length 247;  
Best Local Similarity 74.4%; Pred. No. 3.1e-85;  
Matches 186; Conservative 27; Mismatches 32; Indels 5; Gaps 2;  
  
QY 1 MEGTFTSPFDSQASRNWSVDSLKNFROISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 60  
Db 1 MDAFASLFQS---SGKWSHDSLKNFROISPAVQSHLKNVYLSLCCALMASAGAYLHLWNI 57  
  
QY 61 WNIIGLLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGINFDPISV 120  
Db 58 WNIIGLLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGINFDPISV 117  
  
QY 121 FVGCNAVFCFSAAMARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 180  
Db 118 ISAFVGSALAFACFSAALVARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 177  
  
QY 181 LYFGLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKE 240  
Db 178 LYFGLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKE 237  
  
QY 241 --EKKKRRN 248  
Db 238 KNEKKKRRD 247  
|||||

## RESULT 4

US-10-167-015-18  
; Sequence 18, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Jchal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; FILE REFERENCE: 1388  
; CURRENT APPLICATION NUMBER: US/10/167,015  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,478  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-167-015-18

Query Match 75.1%; Score 955; DB 9; Length 261;  
Best Local Similarity 73.3%; Pred. No. 2.2e-84;  
Matches 178; Conservative 36; Mismatches 27; Indels 2; Gaps 1;  
  
QY 6 SPFDSQ--SASRNWSVDSLKNFROISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 63  
Db 3 TPNSSOSSSSRSRWSYDLKNFROISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 62  
  
QY 64 GGLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGINFDPISVFGA 123  
Db 63 GGLTTTLAGISGSMVWLLSTPPEEQKRLSLLMASALFQASIGPLIELDLAIDPSLIVSA 122  
  
QY 124 FVGCNAVFCFSAAMARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 183  
Db 123 FVATSLAFACFSAALVARREYLYLGGLLSSGVSLFLFHLFASIFGGSMAVFKFELYF 182  
  
QY 184 GLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKKE 243  
Db 183 GLLVFGYIVFDTOEIIIEKAHLGDMYVVKHALTFTDGFAGVFRILIIIMLKNASEKKE 242  
|||||

```
QY 244 KKR 246
Db 243 KKR 245

RESULT 5
US-10-167-015-32
; Sequence 32, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-32

Query Match 69.5%; Score 884.5; DB 9; Length 252;
Best Local Similarity 66.4%; Pred. No. 1.3e-77;
Matches 166; Conservative 36; Mismatches 41; Indels 7; Gaps 2;

QY 6 SFDPQSAS-----NRWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHI 59
Db 3 AFPSASASAPYCGAGSYDSLKNFRQITAVQTHLKVYTLCCALVASAVGAYLHV 62
QY 60 LNWIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGIFDPSI 119
Db 63 VMNIGTLMGCVGSIWLFSPVYERKRYGLLMAAALLEGASVGLVLADEFDPSI 122
QY 120 VFCAFVGCVAFFCFAAAMLRREYLYLGLSSGVSLLFWLHFASSIFGGSMVAFKF 179
Db 123 LVTFVGTAFIAFCFCAAMVARRREYLYLGLSSGVSLLFWLQAGSIFGHSATSPMF 182
QY 180 ELYFGLLVFVGIVFTQBIIEKAHLGDMYVYKHALTLFTDFGAVFVRLIIMLKNASEK 239
Db 183 EYVFGLLIFLGYVYDTQBIIEAHRGDMYVYKHALTLFTDFVAVLVRVLMKNGADK 242
QY 240 -EKKKKRN 248
Db 243 SEDKKRRS 252

RESULT 6
US-10-167-015-34
; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-34

Query Match 69.1%; Score 878.5; DB 9; Length 258;
Best Local Similarity 65.8%; Pred. No. 5.2e-77;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;

QY 1 MEGFTSPFDSQSASR-----NRWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAA 53
Db 1 MDAFYSTTASSSTSSAPYGGGEGYDSMKNFQISPAVQTHLKVYTLCCVALASSAV 60
QY 54 GAYLHILWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
Db 61 GAYLHVWNIGGLTLMGCVGSIWLFSPVYERKRYWLLMAAALLEGASVGLIKLAV 120
QY 114 NPDPSIVFGAFVGCFAVFGCPFAAAMLRREYLYLGLSSGVSLLFWLHFASSIFG-G 172
Db 121 EFDPSILVTFVGTAFIAFCFCAAMVARRREYLYLGLSSGVSLLFWLQFAASIFGHQ 180
QY 173 SMAVEKEELYFGLLVFVGIVFTQBIIEKAHLGDMYVYKHALTLFTDFGAVFVRLIIM 232
Db 181 STSSFMFEVIFGLIFLGNVYDQEVIERAHRGDMYVYKHALTLFTDFVAVLVRVIM 240
QY 233 LKNASEK-EKKKKRN 248
Db 241 LKNAADKSEDKRRKRS 257

RESULT 7
US-10-167-015-6
; Sequence 6, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-6

Query Match 69.1%; Score 878.5; DB 9; Length 285;
Best Local Similarity 65.8%; Pred. No. 5.8e-77;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;

QY 1 MEGFTSPFDSQSASR-----NRWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAA 53
Db 1 MDAFYSTTASSSTSSAPYGGGEGYDSMKNFQISPAVQTHLKVYTLCCVALASSAV 60
QY 54 GAYLHILWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
Db 61 GAYLHVWNIGGLTLMGCVGSIWLFSPVYERKRYWLLMAAALLEGASVGLIKLAV 120
QY 114 NPDPSIVFGAFVGCFAVFGCPFAAAMLRREYLYLGLSSGVSLLFWLHFASSIFG-G 172
Db 121 EFDPSILVTFVGTAFIAFCFCAAMVARRREYLYLGLSSGVSLLFWLQFAASIFGHQ 180
```

QY 173 SMAVFKPELVFGLLVFVGYIVFTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIM 232  
Db 181 STSFMFVYFGLLVFVGYIVFTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIM 240  
QY 233 LKNASEK-EKKKKRN 248  
Db 241 LKNAADKSEDKRRKRS 257

## RESULT 8

US-10-167-015-4  
; Sequence 4, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Johal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; FILE REFERENCE: Thereof  
; CURRENT APPLICATION NUMBER: US/10/167,015  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,478  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-167-015-4

Query Match 67.1%; Score 853; DB 9; Length 252;

Best Local Similarity 65.1%; Pred. No. 1.4e-74;  
Matches 162; Conservative 32; Mismatches 43; Indels 12; Gaps 2;

QY 6 SFFDSQAS-----RNRWSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHI 59  
Db 3 AFFSASSAPYGYGAGGWSYDSLKNFRQITPAVQTHLKVYLTCCALVASAAGAYLHV 62  
QY 60 LWNIGGLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGINFDP 119  
Db 63 VWNIGGLTLMCGSIAWLFVSVYERKRYGLLMAALLEGASVGPLKLAVEFDP 122  
QY 120 VEGAVGCAVVGFCFSAAMLARREYLYLGLLSSGVSLFWLHFASSTFGGSMVVKF 179  
Db 123 LVTAFTVGTATAFACFTGANVARRREYLYLGLLSSGVSLFWLHAGSIFGHSATF 182  
QY 180 ELYFGLLVFVGYIVFTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIMLK- 234  
Db 183 EYVFGLLIFLGVVYVDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIMLK 242  
QY 235 -NASEKEK 242  
Db 243 VCGQEEBE 251

## RESULT 9

US-10-167-015-2  
; Sequence 2, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Johal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; FILE REFERENCE: Thereof  
; CURRENT APPLICATION NUMBER: US/10/167,015

; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,478  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-167-015-2

Query Match 61.8%; Score 786.5; DB 9; Length 250;

Best Local Similarity 64.8%; Pred. No. 3.7e-68;  
Matches 158; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 11 QSASNR---WSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHILNIGLL 67  
Db 7 QSORRRAGSGFESLKRGLHISPAVQSHLKHVYLTCSALAFSALGAYLHILNIGGAL 66  
QY 68 TTMACGSMVWLLSAPPY---QEKRVALLMAALFEGASIGPLIELGINFDPSTVFC 125  
Db 67 TTGCVASIAFLISLPASDQERNRLALLMAALQGSVGPLVDLVDLSRIIVTAFV 126  
QY 126 GCAVFGCFSAAMLARREYLYLGLLSSGVSLFWLHFASSTFGGSMVVKFELYFGL 185  
Db 127 GTAVAFACFSGAAIAKREYLYLGLLSSGVSLFWLHFASSTFGGSMVVKFELYFGL 186  
QY 186 LVFVGYIVFTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIMLKNASEK--BEKK 243  
Db 187 LVFLGYVVFDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRLIIMLKNASEK--BEKK 246  
QY 244 KXER 247  
Db 247 RKXR 250

## RESULT 10

US-10-219-220-273  
; Sequence 273, Application US/10219220  
; Publication No. US20030082724A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: Death and their use in the modification of plant development  
; FILE REFERENCE: 11000.1022c1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 273  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Pinus radiata  
US-10-219-220-273

Query Match 60.7%; Score 772.5; DB 9; Length 255;

Best Local Similarity 60.2%; Pred. No. 8.6e-67;  
Matches 153; Conservative 39; Mismatches 55; Indels 7; Gaps 3;

QY 1 MEGFTSP---FDSQASRNRWSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAY 56  
Db 1 MASVASYVGGFFNQGFHPSWDYNAKMKKISPAVQSHLKHVYLTCSALVTAAGVY 60  
QY 57 LHLWNIGGLTTMACGSMVWLLSAPPYQEKRVALLMAALFEGASIGPLIELGIN 114  
Db 61 LHLNIGGLTGLGACIGSVIGLSVFTSSNNEGRAALLLAAAFKGTATGLPLIDAVIN 120  
QY 115 FDPISVFCVAVGCAVVGFCFSAAMLARREYLYLGLLSSGVSLFWLHFASSTFGGSM 174  
Db 121 IDSSILVSATVGLSLAFACFSAAITARRREYLVFGLLGSIGSILMWLQASSIFGSS 180

QY 175 AVFKEELVGLVFGYIVFDTOIEIKAHLGDMYVVKHALTLFTDFGAVFVRILIMLK 234  
DB 181 AIYTEIVFGLVFGYIVFDTOIEIKAHLGDMYVVKHALTLFTDFGAVFVRILIMLK 240  
QY 235 NA-SEKKEKKRR 247  
DB 241 NADSKREGKKRR 254

RESULT 11  
US-10-219-220-87  
; Sequence 87, Application US/10219220  
; Publication No. US20030082724A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of plant development  
; FILE REFERENCE: 11000.1022c1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 87  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Pinus radiata  
US-10-219-220-87

Query Match 54.1%; Score 688.5; DB 9; Length 213;  
Best Local Similarity 64.6%; Pred. No. 8.8e-59;  
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;

QY 39 QVYLTCCALVASAAGAYLHILNIGLLTTCMACGSMVLLSAP--PYOEQKRVALLMA 96  
DB 1 RYLSLSALVTAAGLVYHLLNIGLLTGLACIGSVIGLLSVTSSNNEKGAALLA 60

QY 97 AALFGASIGPIELIENFDPSIVFGAVGCVFVGCPSAAMLARRRYLYIGLLSSG 156  
DB 61 AAFAFGATLGLPIDAVINIDSSILVSFAVGTSLAFACPSAAAITARRRYLYFLGGLSG 120

QY 157 VSLFWLHFASIFGSGMAVRKFELYFGLLVFGYIVFDTOIEIKAHLGDMYVVKHALT 216  
DB 121 ISLMLWLQASSIFGSSAIYTFEYFGLLVFLGLYIFDTOMIEKADHDYDYLKSLD 180

QY 217 LFTDFGAVFVRILIMLNA-SEKKEKKRR 247  
DB 181 LFTDFGAVFVRILIMLNA-SEKKEKKRR 212

RESULT 12  
US-10-219-220-88  
; Sequence 88, Application US/10219220  
; Publication No. US20030082724A1  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of plant development  
; FILE REFERENCE: 11000.1022c1  
; CURRENT APPLICATION NUMBER: US/10/219,220  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 88  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Pinus radiata

## US-10-219-220-88

Query Match 39.3%; Score 499.5; DB 9; Length 140;  
Best Local Similarity 66.2%; Pred. No. 9.1e-41;  
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGFTSPFDSQASRNRSYDSLKNFRQISPLVOTHLKQVYLTCCALVASAAGAYLHIL 60  
DB 1 MDAFASLPQS---SGKWSHDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHLM 57

QY 61 WNIIGLLTTCMACGSMVLLSAPPYOEQKRVALLMAALFEGASIGPLIELINFDPSIV 120  
DB 58 LNIIGLLTTCMACGSMVLLSAPPYOEQKRVALLMAALFEGASIGPLIELIAIKVDFSI 117

QY 121 FGAIVGCAVFGCFSAAMLARRRYLYLGG 151  
DB 118 ISAFVGSALAFACFGAA-----CWLGG 140

## RESULT 13

US-10-167-015-8  
; Sequence 8, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Jhal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 1388  
; CURRENT APPLICATION NUMBER: US/10/167,015  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 141  
; TYPE: PRT  
; ORGANISM: zea mays  
US-10-167-015-8

Query Match 38.1%; Score 484.5; DB 9; Length 141;  
Best Local Similarity 67.4%; Pred. No. 2.6e-39;  
Matches 93; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 112 GINFDPSIVFGAVGCAVFGCFSAAMLARRRYLYLGGSSGVLFWLHFASIFG 171  
DB 4 GCFPSLSILVTFVGTAFACFTGAAMVARRRYLYLGGSSGVLFWLHFASIFG 63

QY 172 GSMVAFKPELYFGLLVFGYIVFDTOIEIKAHLGDMYVVKHALTLFTDFGAVFVRILII 231  
DB 64 HSATSFMFEVYFGLLVFGYIVFDTOIEIKAHLGDMYVVKHALTLFTDFGAVFVRILII 123

QY 232 MLKNASEK-EKKEKKRR 248  
DB 124 MLKNAKSEKEDKKEKKRR 141

## RESULT 14

US-09-925-302-516  
; Sequence 516, Application US/09925302  
; Patent No. US2002004941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P1104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR FILING DATE: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08



Search completed: May 25, 2003, 12:31:16  
Job time : 55 secs

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; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 516
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-516

Query Match      38.0%; Score 483.5; DB 10; Length 255;
Best Local Similarity 41.1%; Pred. No. 6.5e-39;
Matches 102; Conservative 54; Mismatches 79; Indels 13; Gaps 5;

QY 3 GFTSFFDSQASNRNWSYSLKNPQISPLVQTHLKQVYLTCCALVASAAGAYLHILWN 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 GTWNIFD-----RKINFDAALKFSHITPSTQOHLKKVYASFALCNMFVAAGAYVHMVTH 70
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 63 I--GGLTWTMACGSMYWLISAPPYQ--EOKRVALLMAAALFEGASIGGLIELGINFOPS 118
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 71 FIQAGLSALGSLILMLWATPHSHETEQKRLGLLAGFAFLTGVGLGPALEFCIAVNPFS 130
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 119 IVFGAFVGCVAVFCFSAAMLARREYLYLGGLLSGVSLFLFWLHFASIFGGSMAVFK 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 131 ILPTAFMTAMIFCTFTLSALYARRSYLFLGGILMSALLL--LSSLGNVFFGSIWLFQ 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 179 FELYGLLVFGYIVFDTQELIEKAHAGDMYVKHALTLFTDFGAVFVRILIIIMLKNAE 238
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 ANLYVGLVVMCGFVFDITQIIIEKAERGDDQYIWHCIDLFDLFIIVFRKLMILAWN--E 247
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 239 KEEKKKR 246
   | : | : | :
Db 248 KDKKKEK 255

RESULT 15
US-10-167-015-20
; Sequence 20, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Jhal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 78
; TYPE: PRT
; ORGANISM: glycine max
US-10-167-015-20

Query Match      26.7%; Score 339; DB 9; Length 78;
Best Local Similarity 80.8%; Pred. No. 1.4e-25;
Matches 63; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 171 GGSMAVFEFLYFGLVFGYIVFDTQELIEKAHAGDMYVKHALTLFTDFGAVFVRILI 230
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 GGSIALFRELFLYFGLVFGYIVFDTQELIERAFGLDLYVKHALTLFTDLAIFVRILI 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 231 IMLKNAEKEEKKKRN 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 IMLKNSERNKKKKRD 78
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2003, 12:16:44 ; Search time 43 Seconds  
(without alignments)

554.450 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDSQASARNWSY.....LIIMLNKASEKKEKKKKRN 248

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023.5	80.5	247	2	T52449
2	479	37.7	236	2	S42069
3	472	37.1	261	2	E71445
4	472	37.1	262	2	A85197
5	471.5	37.1	237	2	I38334
6	170.5	13.4	219	2	A10628
7	157.5	12.4	219	2	D85624
8	157.5	12.4	219	2	F90760
9	157.5	12.4	219	2	S07180
10	144	11.3	266	2	T41414
11	143.5	11.3	342	2	T34438
12	143	11.2	297	2	S63281
13	136.5	10.7	245	2	A83484
14	130.5	10.3	238	2	E81729
15	128.5	10.1	238	2	E71457
16	128	10.1	236	2	A10142
17	124.5	9.8	239	2	T48120
18	124	9.7	231	2	A75422
19	123.5	9.7	231	2	D81441
20	122	9.6	234	1	B48415
21	122	9.6	234	2	H90736
22	122	9.6	234	2	A85587
23	121.5	9.6	239	1	Q08E35
24	120	9.4	222	2	S38835
25	120	9.4	422	2	H44899
26	114.5	9.0	220	2	A64141
27	114	9.0	227	2	G81014
28	113	8.9	223	2	D82210
29	112.5	8.8	230	1	H54634

30 112 8.8 232 2 AH0954 probable membrane  
31 109.5 8.6 230 2 F71879 hypothetical prote  
32 109 8.6 260 2 B97681 hypothetical prote  
33 109 8.6 260 2 AI2905 conserved hypothet  
34 108.5 8.5 236 2 H71724 hypothetical prote  
35 106 8.3 659 2 AB1293 ABC transporter (p  
36 104 8.2 203 2 S53708 N-methyl-D-aspart  
37 103.5 8.1 670 2 AH1664 ABC transporter (p  
38 101.5 8.0 225 2 AG1350 hypothetical prote  
39 101.5 8.0 236 2 E97723 hypothetical prote  
40 101.5 8.0 238 2 H86611 transport permease  
41 101.5 8.0 238 2 A72013 transport permease  
42 99.5 7.8 225 2 AB1721 hypothetical prote  
43 99.5 7.8 248 2 T01080 hypothetical prote  
44 99 7.8 231 2 D97248 conserved membrane  
45 98.5 7.7 511 2 JC7692 oligodendrocyte tr

#### ALIGNMENTS

##### RESULT 1

T52449  
Bax inhibitor-1 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 03-Nov-2000  
C:Accession: T52449  
Rikawai, M.; Pan, L.; Reed, J.C.; Uchimiya, H.  
FEBS Lett. 464, 143-147, 1999  
A:Title: Evolutionally conserved plant homologue of the Bax Inhibitor-1 (BI-1) gene car  
A:Reference number: Z26078  
A:Accession: T52449  
A:Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-247 <KAW>  
A:Cross-references: EMBL:AB025927; PIDN:BA089541.2  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Gene: AtBI-1  
C:Function:  
A:Description: suppresses cell death induced by Bax  
C:Superfamily: human testicular protein TEGP

Query Match 80.5% Score 1023.5; DB 2; Length 247;  
Best Local Similarity 77.4%; Pred. No. 1.4e-85;  
Matches 192; Conservative 31; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MEGTSPFDSQASARNWSYDSLKNFRQISPLVQTHLKQVYLTLCALVASAGAYLHL 60

Db 1 MDAFSSFFDSQFGSRS-WSYDSLKNFRQISPAVNHLKRVYLTLCALVASAGAYLHL 59

Qy 61 WNIGLLTTCMACGSMYMLLSAPPYQKQKRVALLMAALFEGASIGLIELGINFDPSTV 120

Db 60 WNIGGILTTICIGTMIWLLSCPPYEHQKLSLLFVSAVLGASVGLIKVAIDVDPSIL 119

Qy 121 FGAFCGAVFGCCSAAMLARREYLYLGLSSGVSLFLFWLHPASSIFGGSMVFKEE 180

Db 120 ITAFVGTATAPVCSAAMLARREYLYLGLSSGVSLFLFWLHPASSIFGGSMVFKEE 179

Qy 181 LYFGLLVFGVYIVDFDQIEIKHGLGMDVYVXHALTFDVGAVFVRILIIIMKNASEKE 240

Db 180 LYFGLLIFVGMVVDQIEIKHGLGMDVYVXHSULTFTDFVAVFVRILIIIMKNASDKE 239

Qy 241 EKKKKRN 248

Db 240 EKKKKRN 247

##### RESULT 2

S42069

TEGP protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

Query Match 37.1%; Score 472; DB 2; Length 261;

```
Query Match 37.1%; Score 471.5; DB 2; Length 237;
Best Local Similarity 42.2%; Pred. No. 1.9e-35;
Matches 98; Conservative 51; Mismatches 76; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTLCALVASAGAYLHILWNI--GGLTTWACGSM 76
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 9 NFDALLKFSHTPTQQHLLKQVYALCMVAAGAYVMVTHFIQAGLLSALGSJLM 68
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 77 VMLLSAPPYQ--EQKRVALLMAALFEGASIGPLIELGINFDPISVFGAFVGCVF 134
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 63 INLMATPSHETEQRKELGLLAGFAFLTGVGIGPALEFCIAVNPISILPTAWGTAMITCF 128
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 135 SAAMALARREYLYLGGLLSSGVSLFLWHPASSIFGSGMAVFKFELYFGLLVFGVIVF 194
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 129 TLSALYARRSYLFGGILMSALSLL--LSSLGNVFGSIWPFQANLYVGLVVMCGFVLV 187
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 195 DTQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRIILIIMLKVASKEKKKKR 246
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 188 DTQLIIEKAHGDQYIWHCIDLDFLDTIVRKMLMILLAWN--EKDKKKKK 237
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
A:Accession: A10628
A:Title: probable membrane protein STY112 [imported] - Salmonella enterica subsp. enterica serov.
A:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002
R:Accession: A10628
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: A10628
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08212.1; PID:g16502260; GSPDB:GN00176
C:Genetics:
A:Gene: STY112
A:Superfamily: Escherichia coli ybhL protein

Query Match 13.4%; Score 170.5; DB 2; Length 219;
Best Local Similarity 29.2%; Pred. No. 3.9e-08;
Matches 66; Conservative 42; Mismatches 77; Indels 41; Gaps 11;

QY 27 ROISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGLTTWACGSMVLLSA 82
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 9 RDRSLLSTHKVLRNTYFLLSLTAFSAITASTVLMPLSPGILTLVGMVGLMFL-- 65
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 83 PPYQ--EQKRVALLMAAL--FEGASIGPLIELGINFDPISVFG--AFVGCVAVFGCFSA 138
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 66 --TYKTANKPVGILSAFAFTGFGYILGILNAYLSAGMGDVIGALGATLVFFCCS--AY 123
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 139 MLARREYLYLGGLLSSGVSLFL--WHPASSIFGSGMAVFKFELYFGLLV 186
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 124 VLTTRKDSFLGGLMAGIVVYLVIGVANIQLPALHLAIS-----AVF-----IL 170
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 187 VFVGYIVFTQRIIEKAHLGDMYVVKHALTLFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 171 ISSGALLYFETSNII--HGGETNYIRATVSVLYSVLYNIFVLSLSIL 213
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
A:Accession: D85624
A:Title: probable carrier/transport protein yccA [imported] - Escherichia coli (strain O157:H7, s
A:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Aug-2002
R:Accession: D85624
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: D85624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <STO>
A:Cross-references: GB:AE005174; NID:g12514158; PIDN:AA55456.1; GSPDB:GN00145; UWGP:Z1
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yccA
C:Superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;
Best Local Similarity 26.7%; Pred. No. 5.9e-07;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRNSYDSLKNFRQISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGL 67
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITASTVLMPLSPGLI 53
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 TTMACGSMVWLLSAPPYQEQKRVALLMAAL--FEGASIGPLIELGINFDP--PSIVFGAF 124
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGFGYILGILNAYLSAGMGDVIA 110
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 VGCVAVFGCFSAAMALARREYLYLGGLLSSGVSLFL--WHPASSIFGG 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 111 GGTALVFFCCS--AVLTTRKDSFLGGLMAGIVVYLVIGVANIQLPALHLAIS-- 165
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 173 SMAVFKELYFGLLVFGVIVFTQRIIEKAHLGDMYVVKHALTLFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 166 --AVF-----ILISSGAILFETSNII--HGGETNYIRATVSVLYSVLYNIFVLSLSIL 213
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 8
A:Accession: F90760
A:Title: probable carrier/transport protein ECs1054 [imported] - Escherichia coli (strain O157:H
A:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Aug-2002
A:Accession: F90760
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ger
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA34477.1; PID:g13360514; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1054
C:Superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;
Best Local Similarity 26.7%; Pred. No. 5.9e-07;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRNSYDSLKNFRQISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGL 67
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITASTVLMPLSPGLI 53
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 TTMACGSMVWLLSAPPYQEQKRVALLMAAL--FEGASIGPLIELGINFDP--PSIVFGAF 124
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGFGYILGILNAYLSAGMGDVIA 110
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 VGCVAVFGCFSAAMALARREYLYLGGLLSSGVSLFL--WHPASSIFGG 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 111 GGTALVFFCCS--AVLTTRKDSFLGGLMAGIVVYLVIGVANIQLPALHLAIS-- 165
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 173 SMAVFKELYFGLLVFGVIVFTQRIIEKAHLGDMYVVKHALTLFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Db 166 --AVF-----ILISSGALLPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

RESULT 9  
S07180  
probable glutamate receptor ycca - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 01-Mar-2002  
C:Accession: S07180; A64838  
R:Tamura, F.; Nishimura, S.; Ohki, M.  
EMBO J. 3, 1103-1107, 1984  
A:Title: The E. coli divE mutation, which differentially inhibits synthesis of certain P  
A:Reference number: S07180; PMID:84236106; PMID:6376117  
A:Accession: S07180  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-219 <TAV>  
A:Cross-references: EMBL:X00547; NID:g41283; PIDN:CAA25218.1; PID:g41284  
A:Experimental source: strain W3110  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; PMID:97426617; PMID:9278503  
A:Accession: A64838  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-219 <BLAT>  
A:Cross-references: GB:AE000199; GB:U00096; NID:g1787202; PIDN:AAC74056.1; PID:g1787205;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: ycca  
A:Map position: 22 min  
C:Superfamily: Escherichia coli ybhL protein  
C:Keywords: transmembrane protein  
F:26-42/Domain: transmembrane #status predicted <TM1>  
F:43-59/Domain: transmembrane #status predicted <TM2>  
F:75-91/Domain: transmembrane #status predicted <TM3>  
F:105-121/Domain: transmembrane #status predicted <TM4>  
F:128-154/Domain: transmembrane #status predicted <TM5>  
F:162-178/Domain: transmembrane #status predicted <TM6>  
F:200-216/Domain: transmembrane #status predicted <TM7>

Query Match 12.4%; Score 157.5; DB 2; Length 219;  
Best Local Similarity 27.0%; Pred. No. 5.9e-07;  
Matches 65; Conservative 46; Mismatches 77; Indels 53; Gaps 12;

QY 12 SASRNRWSYSLKFRQISPLVQTH--LKQVY--LTLCCALVASAAGAYLHILNIGILL 67  
Db 6 SSSHDRTS-----LSTHVKLVNTVFLSLTSLTAFSAITATASTVMLPSPGLI 53

QY 68 TTMACGSMWLLSAPPYQ-EQKRVALLMAAL--FEGASIGFLIELGINFD-PSIVFGA 123  
Db 54 LTLVGMVGLMFL---TYTKANKPTGIIISAFPTGFLGILGILNTVLSAGMGDVIAA 109

QY 124 FVCAVVGCGFSAAMLARREVLVGLLSGVSLFF-----WLHFASSIFG 171  
Db 110 LGGTALVFFCCS-AYLITTRKMSFLGMLMAGIVVVLIGMVFANIFLQPALHLAIS--- 165

QY 172 GSMVAFKFLYFGLLVFGVYIVFDTCETIIIEKAHLGDMVDYVXHALFTDFGAVFVRIILI 231  
Db 166 --AVF-----ILISSGALLPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSI 212

QY 232 M 232  
Db 213 L 213

RESULT 10  
T41414  
probable receptor-associated protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T41414  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z21954  
A:Accession: T41414  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-266 <WOO>  
A:Cross-references: EMBL:AL031798; PIDN:CAA21193.1; GSPDB:GN00068; SPDB:SPCC576.04  
A:Experimental source: strain 972h-; cosmid c576  
C:Genetics:  
A:Gene: SPDB:SPCC576.04  
A:Map position: 3

Query Match 11.3%; Score 144; DB 2; Length 266;  
Best Local Similarity 24.9%; Pred. No. 1.2e-05;  
Matches 65; Conservative 39; Mismatches 95; Indels 62; Gaps 14;

QY 10 SOSARNWSYSLKFRQISPLVQ-----THLKQVYLTLCAL-VASAAGA--YLHI 59  
Db 29 NESATEN-----PAVDQFNKTPVAECAKSRMAFLRKVYAILTAQLFVTSLFGGIFVLP 84

QY 60 LWN-----IGGLTTMACGSMWLLSAPPYQEKRVALLMAALFEGASIGPL 108  
Db 85 ASFVQVQHPDFLILNFFISLVLPF-----LIMKPYSPRYNIFLFLTALEGLILGTA 139

QY 109 IELGNFDPSPVIFGAFVGCAGVFCFSA--AAMLARREVLVGLLSGV-----SLL 160  
Db 140 ITF--FSARIILEAVF---ITLGVFVALTAFTQSKWDFSRGLGFLYVLSLILITPLI 193

QY 161 FWL---HFASSIFGSMVAFKFLYFGLLVFGVYIVFDTCETIIIEKAHLGDMVDYVXHALT 216  
Db 194 FPFVSTPFDMAFAG-----FGTLVFCGYILFDYINILHR--YSPERFIMSSLM 241

QY 217 LFTDFGAVFVRILII--MLKN 235  
Db 242 LYLDIFNLFIQLILGMLQN 262

RESULT 11  
T34438  
hypothetical protein K11H12.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T34438  
R:Bradshaw, H.  
submitted to the EMBL Data Library, February 1997  
A:Description: The sequence of C. elegans cosmid K11H12.  
A:Reference number: Z21526  
A:Accession: T34438  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-342 <BRA>  
A:Cross-references: EMBL:U86168; PIDN:AAC24402.1; GSPDB:GN00022; CBSP:K11H12.8  
A:Experimental source: strain Bristol N2; clone K11H12  
C:Genetics:  
A:Gene: CBSP:K11H12.8  
A:Map position: 4  
A:Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2

Query Match 11.3%; Score 143.5; DB 2; Length 342;  
Best Local Similarity 23.7%; Pred. No. 1.8e-05;  
Matches 51; Conservative 47; Mismatches 86; Indels 31; Gaps 8;

QY 42 LTLCCALVASAAGAYLHILNIGLLTTMACGSMWML-LSAPPYQEKRVALLMAAL- 99  
Db 126 LTAVSGVAASRSAAIMRLTAG-GGNMSLFGTMAAMIASGMARSIDYESTVAKELAWALH 184

QY 100 --FEGASIGFLIELGINFDPSIVFGAFVGCAGVFCFSAAMLARREVLVGLLSGV 157  
Db 185 CGVLGAVAPLCFMA---GPVLTAAWYTAGIV--GGSATATAPSEKFLMMSGPLAMGF 240

QY 158 SLLFWLHFAS-----SIFGSMVAFKFLYFGLLVFGVYIVFDTCETIIIEKA----- 203

```
Db 241 GVVFVANICAFPLPGSGALGASLA--STVVYGGILFSAFLYDQRLVKKAENHPHSSQ 298
QY 204 -----HLGDMYVVKHALTFTDFGAVFVRILIM 232
Db 299 LYGSDMQIRSDPINAQMSIYDNLNIFRLVIM 333

RESULT 12
S63281
probable membrane protein YNL305c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0405
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
A:Accession: S63281
A:Residues: 1-297 <MAU>
A:Molecule type: DNA
A:Cross-references: EMBL:Z71581; NID:g1302402; PID:e239757; PID:g1302403; MIPS:YNL305c
A:Experimental source: strain 5288C
R:Maurer, K.C.T.; Urbanus, J.H.M.; Plant, R.J.
Yeast 11, 1303-1310, 1995
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a
C: and a novel putative serine/threonine protein kinase gene.
A:Reference number: S60394; MUID:96132033; PMID:8553702
A:Accession: S60395
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-297, 'D' <MAW>
A:Cross-references: EMBL:U23084
R:Maurer, K.T.C.
submitted to the EMBL Data Library, March 1995
A:Reference number: S66127
A:Accession: S66127
A:Molecule type: DNA
A:Residues: 1-297 <MAP>
A:Cross-references: EMBL:U23084; NID:g1050853; PID:g1050855
C:Genetics:
A:Cross-references: SGD:S0005249
A:Map position: 14L
C:Keywords: transmembrane protein
F:86-102/Domain: transmembrane #status predicted <TM1>
F:173-189/Domain: transmembrane #status predicted <TM2>
F:212-228/Domain: transmembrane #status predicted <TM3>
F:238-254/Domain: transmembrane #status predicted <TM4>
F:271-287/Domain: transmembrane #status predicted <TM5>

Query Match 11.2%; Score 143; DB 2; Length 297;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;

QY 31 PLV-OTHLKQVYLTCCALVASAAGY-----LHI-LWNIIGLLTTMACWGS 75
Db 44 PIIRQPMKHYVLSLSCQLLASLFCYVASTSLQNFIMSHIALFICVMVSLVSC--- 100
QY 76 MWLLSAP-----PYEQKR-----VALLMAALFEGA 103
Db 101 -IWLAVSRPRDEYASVPEPLLTGSSSEPAEQRLPWVLSYKQKLTLLSIFTLSEAY 159
QY 104 SIGPIELGINPDSIVGAFVGCFAVGCFAAAMLARREYLYLGLLSSGVSLFLWL 163
Db 160 CLS-LVTLA--YKQTVLSALITIVVGVSLTALSER-----FENVLSATSIYWL 210
QY 164 HF-----ASSIFGSGMAVFKFELYFGLL---VPGYIVFDTOEIEKAHLGDMY 210
Db 211 NWGLTWICWGLTALLFGWNTHSSKNFLYGMGLLTAFLYDITQILFKVY--PDEE 268
QY 211 VKHALTFTDFGAVFVRILIMLKNAE 238
Db 269 VRCAWMLYLDIVNLFSLIRI--LANSND 295

us-09-955-526-4.rpr

RESULT 13
AE3484
integral membrane protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
A:Accession: AE3484
R:Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Muter, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella meliter
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KUR>
A:Cross-references: GB:AE008917; PID:AA153040.1; PID:g17983899; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1859
A:Map position: I
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.7%; Score 136.5; DB 2; Length 245;
Best Local Similarity 29.1%; Pred. No. 5.3e-05;
Matches 64; Conservative 31; Mismatches 76; Indels 49; Gaps 10;

QY 55 AYHLILMN---IGGLTTMACMSMWLLSAPPYQB-----QKRVALLMA--AALF---- 100
Db 29 SYMLGVYVNMVAIGLAVTGLAAGFAVLAQSNPAFQQLFASPLRWVIMLAPLAAPVFLSF 88
QY 101 -EGASIG-----PIELGINPDSIVGAFVGCFAVGCFAAAMLARREYLY 148
Db 89 RIQSLSVGTACAIWGYAALVGLSL-----SSIFVTGQSIVTFFVTAASFGALSLYGY 144
QY 149 -----LGGLSSGVSLFLFWLHFAS--SIFGSMVAFKELYFGLLVFVGVIVFDTOE 198
Db 145 TTKRNLSANGSFLMWG--LFGILASVNVNIFLGSALQFAISVIGLVIFAGLTAYDTQE 201
QY 199 IIEKAHLGD-----MDYVKHALTFTDFGAVFVRILIM 232
Db 202 IKEMYEGDAADTQGRKIVNGALRLYLDFINMFELQFM 241

RESULT 14
EB1729
conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
A:Accession: EB1729
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: EB1729
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <TET>
A:Cross-references: GB:AE002287; GB:AE002160; NID:g7190237; PID:AAF39078.1; PID:g7190;
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0206
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.3%; Score 130.5; DB 2; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00018;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;

QY 20 YDSLKNFQISPLVQTHLKQVY-----LTLCALVASAAGY--LHLWNIGLLIT 69
Db 4 YD--RDYTDQSRLPFTSSRVYGMWMTAGLAVTALTSGLYATGATYTLFSLW----WVWC 57
```

```
QY 70 MACMG-----SMVWLLSAPPYQOKRVALLMAAALFEGASIGPLIEL-GINFDPSPVIFG 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 FATLGVSFYIAQIQKLSVPVAV-----MGLFLAYSILEGMFFGTLVPVYAAQFGGCVVWA 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 AFVGCVVFGCFSAAMLAR-----RREYLYGGLSSGVSLFLFWLHFASSIFGGSMA 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 AFGSAAVIFGLSAAAYGAFTKSDTQTHRIIMLALIGLWV--ISLGF--LVVSLFTPEML 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 VFKEPELYGGLLVFVGIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MYLLICYLGLIIFVGLTVVDAQSIRRVARSVGDHGDLSYKLSLIMALQYCNVIMIFWYL 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 LII 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 LQI 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
E71467
Probable transport permease - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71467
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trad
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71467
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-238 <ARN>
A;Cross-references: GB:AE001354; GB:AE001273; NID:G3329280; PIDN:AAC68416.1; PID:G332928
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ycca
C;Superfamily: Escherichia coli ybhL protein

Query Match 10.1%; Score 128.5; DB 2; Length 238;
Best Local Similarity 25.9%; Pred. No. 0.00028;
Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;

QY 20 YDSLKNFRQISPLVQTHLKQVY-----LTCCALVASAAGAY--LHILWNIGGLTT 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 YD--RDYAQDSRLPGTFSRYGYGMWTAGLAVTALTSLGLYATGAYRALPFMW-----WIWC 57
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 MACMG-----SMVWLLSAPPYQOKRVALLMAAALFEGASIGPLIEL-GINFDPSPVIFG 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 FATLGVSFYIAQIQKLSVPVAV-----MGLFLAYSILEGMFFGTLVPVYAAQFGGCVVWA 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 AFVGCVVFGCFSAAMLAR-----RREYLYGGLSSGVSLFLFWLHFASSIFGGSMA 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 AFGSAGIIFGLSAAAYGAFTKNDLTQTHRIIMLALVGLWV--ISLAFLL--VSLFTPEML 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 VFKEPELYGGLLVFVGIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MYLLICYLGLIIFVGLTVVDAQSIRRVARSVGDHGDLSYKLSLIMALQYCNVIMIFWYL 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 LII 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 LQI 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: May 25, 2003, 12:23:46  
Job time : 44 secs

GenCore version 5.1.5  
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OM protein - protein search, using sw model

Run on: May 25, 2003, 11:26:54 ; Search time 36 seconds  
(without alignments)  
285.726 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTFFDQSASRNWSY.....LIIMLNASEKEKKKKERN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023.5	80.5	247	1 BIL_ARATH	Q91d45 arabidopsis
2	876.5	68.9	247	1 BIL_ORISA	Q9mbd8 oryza sativ
3	481.5	37.9	237	1 BIL_HUMAN	P55061 homo sapien
4	481.5	37.9	237	1 BIL_PAROL	Q91a79 paralichthy
5	479	37.7	236	1 BIL_RAT	P55062 rattus norv
6	312	24.5	245	1 BIL_DROME	Q9vsh3 drosophila
7	165	13.0	345	1 GHIT_HUMAN	Q9h3k2 homo sapien
8	157.5	12.4	219	1 YCCA_ECOLI	P08967 escherichia
9	143	11.2	237	1 YN45_YEAST	P48558 saccharomyc
10	130.5	10.3	238	1 Y206_CHLMU	Q9plal chlamydia m
11	128.5	10.1	238	1 Y819_CHLTR	O84826 chlamydia t
12	125.5	9.9	220	1 Y402_FASMU	Q9cnm5 pasteurella
13	124	9.7	231	1 Y893_DRIRA	Q9rvx8 deinococcus
14	123.5	9.7	231	1 Y236_CAMJE	Q9piq8 campylobact
15	122	9.6	234	1 YBHL_ECOLI	P75768 escherichia
16	121.5	9.6	239	1 Y201_CHMVA	P09723 human cycop
17	120	9.4	232	1 YQ04_PSEAE	Q03268 pseudomonas
18	120	9.4	238	1 ZPRO_MOUSE	Q9da39 mus musculu
19	120	9.4	422	1 YF21_METJA	Q58916 methanococc
20	114.5	9.0	220	1 YCCA_HABIN	P44477 haemophilus
21	114	9.0	227	1 Y420_NIMA	Q9jri0 neisseria m
22	113	8.9	223	1 YD58_VIBCH	Q9ksal vibrio chol
23	112.5	8.4	230	1 Y920_HELPY	Q25578 helicobacte
24	111	8.7	238	1 ZPRO_HUMAN	Q9hc24 homo sapien
25	109.5	8.6	230	1 Y920_HELPY	Q9zkt1 helicobacte
26	108.5	8.5	236	1 Y147_RICPR	Q9zel5 rickettsia
27	97	7.6	545	1 HGTL_CANAL	Q97611 candida alb
28	95	7.5	462	1 NHAC_BACFI	P27611 bacillus fi
29	93.5	7.4	630	1 S6A4_CAVPO	Q35899 cavia porce
30	93	7.3	234	1 YRJB_LACLA	Q9ceub lactococcus
31	92.5	7.3	229	1 Y358_STRPY	Q9alb9 streptococc
32	91	7.2	1124	1 TRPL_DROME	P48994 drosophila
33	90	7.1	1094	1 EMBA_MYCTU	P72060 mycobacteri

RESULT 1  
BIL\_ARATH  
ID BIL\_ARATH STANDARD; PRT; 247 AA.  
AC Q9LD45;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Bax inhibitor-1 (BI-1) (AtBI-1).  
GN BI-1 OR AT5G47120 OR K14A3.7.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20086876; PubMed=10618494;  
RA Kawai M., Pan L., Reed J.C., Uchimiya H.;  
RT "Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1)  
FEBS Lett. 464:143-147(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Leaf;  
RX MEDLINE=2024035; PubMed=10758491;  
RA Sanchez P., de Torres Zabala M., Grant M.;  
RT "AtBI-1, a plant homologue of Bax inhibitor-1, suppresses Bax-induced  
cell death in yeast and is rapidly upregulated during wounding and  
pathogen challenge".  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Kaneko T., Katch T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";  
Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; A5025927; BAA9541.2; --  
CC EMBL; AF208124; AAG35727.1; --  
CC EMBL; A5025609; BAA96107.1; --  
CC InterPro; IPR002199; Bax\_inhbt1.  
CC Pfam; PF01027; UPF0005; 1.  
CC PROSITE; PS01243; B11; 1.  
CC -----



KW Apoptosis; Transmembrane. 80.5%; Score 1023.5; DB 1; Length 247;  
 FT TRANSMEM 58 78 POTENTIAL.  
 FT TRANSMEM 92 112 POTENTIAL.  
 FT TRANSMEM 118 138 POTENTIAL.  
 FT TRANSMEM 145 165 POTENTIAL.  
 FT TRANSMEM 173 193 POTENTIAL.  
 FT TRANSMEM 212 232 POTENTIAL.  
 SQ SEQUENCE 247 AA; 27483 MW; FD3AAEA713363945 CRC64;

Query Match 80.5%; Score 1023.5; DB 1; Length 247;  
 Best Local Similarity 77.4%; Pred. No. 1.3e-69;  
 Matches 192; Conservative 31; Mismatches 24; Indels 1; Gaps 1;

QY 1 MEQFTSFDDQSASRNWSYDSLNKFNQISPLVQTHLKQVYLTLCALVASAAGAYLHL 60  
 DB 1 MDAFSFFDSQPSRS-WYDSLNKFNQISPAVQNLKRVYLTLCALVASAAGAYLHL 59

QY 61 WNTGGLTTMACMGSMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 120  
 DB 60 WNTGGILTTGCGTGMWLLSCPPYEQKRLSLLFVSAVLEGASVGLIKVAIDVPSIL 119

QY 121 FGAFVGCACVFCGSAAMARREYLYLGGLLSSGVSLFWLHFASSIFGSMVAFKPE 180  
 DB 120 ITAFVGTATAFVCFSAAMARREYLYLGGLLSSGLMMLQFASSIFGSSIFKPE 179

QY 181 LYFGLLVFGYIVEDTOEIIIEKAHLGDMYVKHALTLFTDFGAVFVRILIIIMLNASEKE 240  
 DB 180 LYFGLLVFGYVMVDTOEIIIEKAHLGDMYVKHSLTLFTDFVAVFVRILIIIMLNASADKE 239

QY 241 EKKKKRN 248  
 DB 240 EKKKKRN 247

RESULT 2  
 BIL\_HUMAN STANDARD; PRT; 249 AA.  
 ID BIL\_HUMAN STANDARD; PRT; 249 AA.  
 AC Q9MBD8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Bax inhibitor-1 (BI-1) (OsBI-1).  
 GN BIL.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OC NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Yamahoushi;  
 RX MEDLINE=20086876; PubMed=10618494;  
 RA Kawai M., Pan L., Reed J.C., Uchimiya H.;  
 RT "Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1) gene capable of suppressing Bax-induced cell death in yeast."  
 RL FEBS Lett. 464:143-147(1999).  
 CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: UBUIQUITOUS.  
 CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.

-----  
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 CC -----  
 DR EMBL; AB025926; BAA89540.3; -  
 DR InterPro; IPR002139; Bax\_inh1.  
 DR Pfam; PF01027; UPF0005; 1.  
 DR PROSITE; PS01243; BIL; 1.

KW Apoptosis; Transmembrane. 68.9%; Score 876.5; DB 1; Length 249;  
 FT TRANSMEM 39 59 POTENTIAL.  
 FT TRANSMEM 65 85 POTENTIAL.  
 FT TRANSMEM 93 113 POTENTIAL.  
 FT TRANSMEM 119 139 POTENTIAL.  
 FT TRANSMEM 151 171 POTENTIAL.  
 FT TRANSMEM 213 233 POTENTIAL.  
 SQ SEQUENCE 249 AA; 27114 MW; FEA3334173P6D384 CRC64;

Query Match 68.9%; Score 876.5; DB 1; Length 249;  
 Best Local Similarity 66.3%; Pred. No. 1.1e-58;  
 Matches 165; Conservative 40; Mismatches 43; Indels 1; Gaps 1;

QY 1 MEQFTSFDDQSASRNWSYDSLNKFNQISPLVQTHLKQVYLTLCALVASAAGAYLHL 60  
 DB 1 MDAFTSTSAVCAASGWSYDSLNKFNQISPAVQSHLKVLTLCVALAASAVGAYLHVA 60

QY 61 WNTGGLTTMACMGSMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 120  
 DB 61 LNIIGMLTLMGCVSIAWLFSPVFEERKRFGLILLAAALLEGASVGLIKLAVDFOSSIL 120

QY 121 FGAFVGCACVFCGSAAMARREYLYLGGLLSSGVSLFWLHFASSIFGSMVAFKPE 180  
 DB 121 VTAFVGTATAFVCFCAAVAKRREYLYLGGLLSSGUSILLNQFAASIFGHSTGSMFE 180

QY 181 LYFGLLVFGYIVEDTOEIIIEKAHLGDMYVKHALTLFTDFGAVFVRILIIIMLNASEK- 239  
 DB 181 VYFGLLVFGYVMVDTOEIIIEKAHLGDMYVKHALTLFTDFVAVLVRILVIMLNASDKS 240

QY 240 EKKKKRN 248  
 DB 241 EKKKKRN 249

RESULT 3  
 BIL\_HUMAN STANDARD; PRT; 237 AA.  
 ID BIL\_HUMAN STANDARD; PRT; 237 AA.  
 AC P55061; O14938; Q96J50;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).  
 GN BIL OR TEST.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=96015061; PubMed=8530040;  
 RA Walter L., Marynen P., Szpirer J., Levan G., Guenther E.;  
 RT "Identification of a novel conserved human gene, TEST."  
 RL Genomics 28:301-304 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cowling R.T., Birnboim H.C.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Strausberg R.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98325348; PubMed=9660918;  
 RA Xu O., Reed J.C.;  
 RT "Bax inhibitor-1, a mammalian apoptosis suppressor identified by functional screening in yeast."  
 RL Mol. Biol. Cell 1:337-346(1998).  
 CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS.  
 CC -!- SUBUNIT: INTERACTS WITH BCL2 AND BCL-XL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).



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CC -----
DR ENBL; X55855; CAA53470.1; -
DR ENBL; X55856; CAA53471.1; -
DR InterPro; IPR002199; Bax.inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B1; 1.
KW Apoptosis; Transmembrane.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 112 132 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
SQ SEQUENCE 236 AA; 26358 MW; FFA412EC1DC87537 CRC64;
Query Match 37.7%; Score 479; DB 1; Length 236;
Best Local Similarity 43.1%; Pred. No. 4.2e-29;
Matches 100; Conservative 52; Mismatches 72; Indels 8; Gaps 5;
QY 19 SYDSLKNFRQISPLVQPHLKQVYTLCCALVASAAGAYLHLWNI--GGLLTMTACMGSM 76
D 9 NFDALLFSPHTPTQHLKKVYASFALCNFVAAGAYVHVTRFTQAGLLSALGALAIM 68
QY 77 WLLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPISIVFGAFVGCNAVFCG 134
D 69 ICLMATPHSHETEOKRLGLL-AVAFVTGVLGPALELCIAINPSILPTAFMTGIMFTCF 127
QY 135 SAAAMLARRRYLYGLGLLSGVSILFLFWLFPASSIFGGSMAVFKFLYFGLLVFGYIVF 194
D 128 SLSALYARRSYLFLGILSAMSMLP-VSSLGNLFGSILFWLQANLYWGLLVMCGFVLF 186
QY 195 DTQIIKAHIGDMYVYKHALTFTDPAVGVFVRIILIMKNASEKEEKKKKR 246
D 187 DTQIIKAHIGDMYVYKHALTFTDPAVGVFVRIILIMKNASEKEEKKKKR 236
RESULT 6
BIL_DROME STANDARD; PRT; 245 AA.
AC Q9VSH3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable Bax inhibitor-1 (BI-1).
GN CG7188.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de
RA de Fabrics B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders B.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC - FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC - SIMILARITY: BELONGS TO THE B11 FAMILY.
CC -----
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CC -----
DR ENBL; AE003556; AAF50445.1; -
DR FlyBase; FBGN0035871; CG7188.
DR InterPro; IPR002199; Bax.inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B1; 1.
KW Apoptosis; Transmembrane.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 89 109 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
SQ SEQUENCE 245 AA; 27574 MW; 57ACD341C5C94720 CRC64;
Query Match 24.5%; Score 312; DB 1; Length 245;
Best Local Similarity 34.4%; Pred. No. 1.2e-16;
Matches 77; Conservative 48; Mismatches 89; Indels 16; Gaps 5;
QY 31 PLYOTHLKQVYTLCCALVASAAGAYLHI--LWNTIGLLTMTACMGSMWLLSAPPYQEQ 88
D 25 PYVREHLSKVYVGLVGSTAAATANGAMQLMRDLDLG---VLAATAVLVLGLHLYFKDD 80
QY 89 -----KEVALMAALFEGASIGLIELGINFDPISIVFGAFVGCFAAAMLARR 143
D 81 GKNYTRGLMLYAFGSCGQTGLPLGYICSINPAIILISALTGTFTVISLSLALAEQ 140
QY 144 REYLVLGGLSSGVSLFLFWLHPASSIFGGSMAVFKFLYFGLLVFGYIVFDQTQIIKA 203
D 141 GKLYLGLGMLSVINTWALLSLFNMVF-KSYFVQVYVQLVGVFVMAAFIVYDTQIVKRC 199
QY 204 HLGDMYVYKHALTFTDPAVGVFVRIILIMKNASEKEEKKKKR 247
D 200 RGNRDNVQHALDLFFDVLSMFRLRLIIL-----TOKEERKQNER 239

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RESULT 7  
 CHIT\_HUMAN  
 ID CHIT\_HUMAN STANDARD; PRT; 345 AA.  
 AC Q9H3K2; O95894; Q9H0P2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Growth hormone inducible transmembrane protein (Dermal papilla derived protein 2) (Myo21 protein) (PFD010).  
 DE CHITM OR DERP2.  
 GN CHITM OR DERP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Dermal papilla;  
 RA Ikeda A., Yamashita M., Yoshimoto M.;  
 RT "Molecular cloning of a dermal papilla derived gene.";  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mei G., Yu W., Gibbs R.A.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Mao Y.M., Xie Y., Mu Z.M., Li Y., Huang Y.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA MEDLINE=21154917; PubMed=11230166;  
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,  
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,  
 RA Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Pouska A.;  
 RT "Towards a catalog of human genes and proteins: sequencing and  
 RT analysis of 500 novel complete protein coding human cDNAs.";  
 RL Genome Res. 11:422-435 (2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Urinary bladder;  
 RA Strauberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB009685; BAA3049.1; -  
 DR EMBL; AF131820; AAD20052.1; -  
 DR EMBL; AF060923; AAG43135.1; -  
 DR EMBL; AL136713; CAB66648.1; -  
 DR EMBL; BC010354; AAH10354.1; -  
 DR Genew; HGNC:17281; CHITM.  
 DR InterPro; IPR002199; Bax\_inhbt1.  
 DR Pfam; PF01027; UPF0005; 1.  
 KW Transmembrane.  
 FT TRANSMEM 83 103 POTENTIAL.  
 FT TRANSMEM 126 146  
 FT TRANSMEM 160 180 POTENTIAL.  
 FT TRANSMEM 191 211 POTENTIAL.  
 FT TRANSMEM 214 234 POTENTIAL.

FT TRANSMEM 245 265 POTENTIAL.  
 FT TRANSMEM 272 292 POTENTIAL.  
 FT CONFLICT 4 4 A -> V (IN REF. 4).  
 FT CONFLICT 64 64 E -> G (IN REF. 3).  
 FT CONFLICT 74 74 I -> M (IN REF. 4).  
 FT CONFLICT 118 118 Q -> R (IN REF. 4).  
 SQ SEQUENCE 345 AA; 37205 MW; 809FAED86A9CD98E CRC64;  
 Query Match 13.0%; Score 165; DB 1; Length 345;  
 Best Local Similarity 26.3%; Pred. No. 1.4e-05;  
 Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;  
 QY 36 HLKQVYITLCCALVASAGAYLH--ILWNI---GGLLT---TWACMGSMVWLLSAPPYQE 87  
 DB 125 HSTYITLGSIGTALSAIAISRTPLVLMFMFMVGRGWTIGVTPFAAMVGAGMLVRSIPYDQ 184  
 QY 88 Q---KRVALLMAALFEGASIGPLIELGINFDPSIVFGAFVGCVVFGCFSAAAMLARR 144  
 DB 185 SPGPKHLAWLLHSGVM-GAVVPLTILG---GELLRAAWYTAGIV-GGLSTVAMCAPSE 239  
 QY 145 EYVLGGLSSGVSLFLWLFASSIFGGM-----AVFKFELYGLLVFGYIVF 194  
 DB 240 KFLNMGAPLGVGLGV----FVSSL--GSMFLPTTVAGATILYSVAMYGGLVLFNSFLY 293  
 QY 195 DTQBIIEKAHLGDM-----DYVKHALTLTDFGAVFVRILIMLKNASEKE 240  
 DB 294 DTQKVIKRAVSPMYGVQKYDPINSLMSIYMDTLNIFMRVATMLATGGNRKK 345  
 RESULT 8  
 YCCA\_ECOLI  
 ID YCCA\_ECOLI STANDARD; PRT; 219 AA.  
 AC P06957;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein ycca.  
 GN YCCA OR B0970.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia  
 OC Escherichia  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84236106; PubMed=6376117;  
 RA Tamura F., Nishimura S., Ohki M.;  
 RT "The E. coli dive mutation, which differentially inhibits synthesis  
 RT of certain proteins, is in TENASEr1";  
 RL EMBL J. 3:1103-1107 (1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474 (1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map";  
 RL DNA Res. 3:137-155 (1996).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

```

CC -I- SIMILARITY: BELONGS TO THE B11 FAMILY. STRONG, TO H.INFLUENZAE
CC HI0044.
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CC -----
DR EMBL: X00547; CAA35218.1; -.
DR EMBL: AE000199; AAC74056.1; -.
DR EMBL: D90734; BAA35735.1; -.
DR PIR: S07180; S07180.
DR EcoGene: EG11113; yccA.
DR InterPro: IPR002199; Bax_inhbt1.
DR Pfam: PF01027; UFF0005; 1.
DR PROSITE: PS01243; B11; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 158 178 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
SQ SEQUENCE 219 AA; 23362 MW; 4F787B853042ACD8 CRC64;

Query Match 12.4%; Score 157.5; DB 1; Length 219;
Best Local Similarity 27.0%; Pred. No. 3.4e-05;
Matches 65; Conservative 46; Mismatches 77; Indels 53; Gaps 12;

QY 12 SASNRWSYSLKNFROISPLVOTH--LKQV--LTLCCALVASAAGAYHLHILNIGGL 67
D 12 SASNRWSYSLKNFROISPLVOTH--LKQV--LTLCCALVASAAGAYHLHILNIGGL 67
D 6 SSSHDRTS-----LLSTHKVLRNTYFLLSUTLAFAITATASTVLMPLSPGLI 53
QY 68 TTMACMSGMVLLSAPPYO-EQKEVALLMAAL--PEGASIGPLIELGINFD-PSIVFGA 123
D 68 TTMACMSGMVLLSAPPYO-EQKEVALLMAAL--PEGASIGPLIELGINFD-PSIVFGA 123
D 54 LTLVGMGLMFL-----TYKTANKPTGIISAFATGFLGVLGILPILNTYLSAGGDVIA 109
QY 124 FVGCVVFGFCFSAAAMLARREYLYLGLLSSGVSLF-----WLHASSIFG 171
D 124 FVGCVVFGFCFSAAAMLARREYLYLGLLSSGVSLF-----WLHASSIFG 171
D 110 LGGTALVFFCCS-AYVLTTRKMSFLGMLMAGIVVVLGWMVANIPLQLPALHLAIS--- 165
QY 172 GSMAVEKELYFGLVFGVIVPTQELIEKAHLGDMVYVGHALTFTDFGAVFVRILLI 231
D 172 GSMAVEKELYFGLVFGVIVPTQELIEKAHLGDMVYVGHALTFTDFGAVFVRILLI 231
D 166 ---AV7-----LTISSGALLFETSNII--HGGETVIRATVSLVSLYNIPLVSLSI 212
QY 232 M 232
D 232 M 232
D 213 L 213

RESULT 9
IN45 YEAST STANDARD; PRT; 297 AA.
ID YN45_YEAST
AC P48558;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 33.6 kDa protein in MCK1-RPS19B intergenic region.
GN YNL305C OR N0405.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96132033; PubMed=8553702;
RA Maurer K.C.T.; Urbanus J.H.M.; Planta R.J.;
RA "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
RT

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RT carrying a ribosomal protein gene cluster, the genes encoding a
RT plasma membrane protein and a subunit of replication factor C, and a
RT novel putative serine/threonine protein kinase gene."
RL Yeast 11:1303-1310(1995).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: U23084; AAC49093.1; -.
DR EMBL: 271581; CAA96233.1; -.
DR SGD: S0005249; YNL305C.
DR InterPro: IPR002199; Bax_inhbt1.
DR Pfam: PF01027; UFF0005; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 271 291 POTENTIAL.
SQ SEQUENCE 297 AA; 33645 MW; 330784DA17152B80 CRC64;

Query Match 11.2%; Score 143; DB 1; Length 297;
Best Local Similarity 24.3%; Pred. No. 0.00053;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;

QY 31 PLV-QTHLKQVLTCCALVASAAGAY-----LHI-LWNIGGLTTMACNGS 75
D 31 PLV-QTHLKQVLTCCALVASAAGAY-----LHI-LWNIGGLTTMACNGS 75
D 44 PIIRQFMKRVYSLSCQLLASFCYASVSTSLQNFIMSHIALFYICMVYSLVSC--- 100
QY 76 MVLLSAP-----PYQEQK-----VALLMAALPEGA 103
D 76 MVLLSAP-----PYQEQK-----VALLMAALPEGA 103
D 101 -IWLAVSPEDYEASVPEPLTGSSEPAEQRLPWVLSYKQKLTLSITLSEAY 159
QY 104 SIQPLIELGINTDPSIVFGAVFGCAVFGCPSAAMLARREYLYLGLLSSGVSLFLWL 163
D 104 SIQPLIELGINTDPSIVFGAVFGCAVFGCPSAAMLARREYLYLGLLSSGVSLFLWL 163
D 160 CLS-LVTLA--YDKQTVLSALLITTVVGVSLTALSER-----FENVLSATSIIYWL 210
QY 164 HF-----ASSIFGSMVAFKPELVFGLL---VFGVIVPTQELIEKAHLGDMY 210
D 164 HF-----ASSIFGSMVAFKPELVFGLL---VFGVIVPTQELIEKAHLGDMY 210
D 211 NWGLWIMIGLTLALFGWNTSHSKFNLYLWGLTALFTLFDITQLIFKQV--PDDE 268
QY 211 VHALTLFTDFGAVFVRILLIIMLNASE 238
D 211 VHALTLFTDFGAVFVRILLIIMLNASE 238
D 269 VRCAMMLYLDIVNLFSLIRI-LANSND 295

RESULT 10
Y206 CHLMU STANDARD; PRT; 238 AA.
ID Y206_CHLMU
AC Q9PLA1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TC0206.
GN TC0206
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D.; Brunham R.C.; Shen C.; Gill S.R.; Heidelberg J.F.;
RA White O.; Hickey E.K.; Peterson J.; Utterback R.; Berry K.; Bass S.;
RA Linher K.; Weidman J.; Khouri H.; Craven B.; Bowman R.; Dodson R.;
RT

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RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
RL pneumoniae A539"; Science 282:754-759(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: BELONGS TO THE BIL FAMILY.  
CC  
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CC  
CC EMBL; AE002287; AAF39078.1; -  
DR TIGR; TC0206; -  
DR InterPro; IPR002199; Bax inhbr1.  
DR Pfam; PF01027; UPF0005; 1.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 22 42 POTENTIAL.  
FT TRANSMEM 49 69 POTENTIAL.  
FT TRANSMEM 78 98 POTENTIAL.  
FT TRANSMEM 105 125 POTENTIAL.  
FT TRANSMEM 141 161 POTENTIAL.  
FT TRANSMEM 166 186 POTENTIAL.  
FT TRANSMEM 208 228 POTENTIAL.  
FT TRANSMEM 238 AA; 26309 MW; 462581D98093657E CRC64;  
SQ SEQUENCE 238 AA; 26309 MW; 462581D98093657E CRC64;  
Query Match 10.3%; Score 130.5; DB 1; Length 238;  
Best Local Similarity 27.2%; Pred. No. 0.0037;  
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;  
QY 20 YSLKNFRISPLVQTHLKQVY-----ITLCCALVASAAGAY--LHLWNIGGLTT 69  
DB 4 YD--RDYQDSRLPGTSSRYGWMTAGLAVTALTSGLYATGAYRALPFWM---WVWC 57  
QY 70 MACMG-----SMWLLSAPPYQKQKRVALLMAALFEGASIGPLIEL-GINFDPSPVIFG 122  
DB 58 FATLGVSFYIQAKQLSVPAV-----MGLFLAYSIVLEGMFFGTMVPYAAQFGGGVWA 112  
QY 123 AFVGCNAVFGCFSAANMLAR-----RREYVYIGLLSSGVSLLFWLHFASSIFGGSMA 175  
DB 113 AFGSAVIFGLSAAYGAFTKSDLTQIHRILMALIGLMV--ISLGF---LVVSLFTMPL 167  
QY 176 VKFELYFGLLVFGYIVFDTCIEIKAHL---GMDY---VKHALTLFTDFGAVFVRI 228  
DB 168 MLLCYLGLIIFVGLTVVDAQSIRRVARSVDGHDLSYKLSLIMALQMYCNVIMIFWYL 227  
QY 229 LII 231  
DB 228 LQI 230  
RESULT 11  
Y819 CHLTR STANDARD; PRT; 238 AA.  
AC O84826;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein CT819.  
GN CT819.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D/UN-3/Cx;  
RX MEDLINE=99000809; PubMed=9784136;  
RA Stephens R.S., Kaimel S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

RA Davis R.W.;  
RT "Genome sequence of an obligate intracellular pathogen of humans:  
RL Chlamydia trachomatis";  
CC Science 282:754-759(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: BELONGS TO THE BIL FAMILY.  
CC  
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CC  
CC EMBL; AE001354; AAC68416.1; -  
DR InterPro; IPR002199; Bax inhbr1.  
DR Pfam; PF01027; UPF0005; 1.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 22 42 POTENTIAL.  
FT TRANSMEM 49 69 POTENTIAL.  
FT TRANSMEM 78 98 POTENTIAL.  
FT TRANSMEM 105 125 POTENTIAL.  
FT TRANSMEM 141 161 POTENTIAL.  
FT TRANSMEM 166 186 POTENTIAL.  
FT TRANSMEM 208 228 POTENTIAL.  
FT TRANSMEM 238 AA; 26264 MW; FD101F7B3867B8E5 CRC64;  
SQ SEQUENCE 238 AA; 26264 MW; FD101F7B3867B8E5 CRC64;  
Query Match 10.1%; Score 128.5; DB 1; Length 238;  
Best Local Similarity 25.9%; Pred. No. 0.0052;  
Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;  
QY 20 YSLKNFRISPLVQTHLKQVY-----LTLCCALVASAAGAY--LHLWNIGGLTT 69  
DB 4 YD--RDYQDSRLPGTSSRYGWMTAGLAVTALTSGLYATGAYRALPFWM---WVWC 57  
QY 70 MACMG-----SMWLLSAPPYQKQKRVALLMAALFEGASIGPLIEL-GINFDPSPVIFG 122  
DB 58 FATLGVSFYIQAKQLSVPAV-----MGLFLAYSIVLEGMFFGTMVPYAAQFGGGVWA 112  
QY 123 AFVGCNAVFGCFSAANMLAR-----RREYVYIGLLSSGVSLLFWLHFASSIFGGSMA 175  
DB 113 AFGSAVIFGLSAAYGAFTKSDLTQIHRILMALIGLMV--ISLAFI---VSLFTMPL 167  
QY 176 VKFELYFGLLVFGYIVFDTCIEIKAHL---GMDY---VKHALTLFTDFGAVFVRI 228  
DB 168 LVLLCYLGLIIFVGLTVVDAQSIRRVARSVDGHDLSYKLSLIMALQMYCNVIMIFWYL 227  
QY 229 LII 231  
DB 228 LQI 230  
RESULT 12  
Y402 PASMU STANDARD; PRT; 220 AA.  
AC Q9CNMS;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein PM0402.  
GN PM0402.  
OS Pasteurella multocida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM70;  
RX MEDLINE=21145866; PubMed=11248100;  
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
RA "Complete genomic sequence of Pasteurella multocida PM70";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

```
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BII FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB060676; AAK02486.1; -
CC InterPro; IPR002199; Bax_inhbt1.
CC Pfam; PF01027; UPF0005; 1.
CC Hypothetical protein; Transmembrane; Complete proteome.
CC TRANSMEM 25 45 POTENTIAL.
CC TRANSMEM 50 70 POTENTIAL.
CC TRANSMEM 74 94 POTENTIAL.
CC TRANSMEM 105 125 POTENTIAL.
CC TRANSMEM 135 155 POTENTIAL.
CC TRANSMEM 158 178 POTENTIAL.
CC TRANSMEM 195 216 POTENTIAL.
CC TRANSMEM 220 AA; 23936 MW; 8EBC2E3FB4B5CDD5 CRC64;
CC SEQUENCE
CC -----
Query Match 9.9%; Score 125.5; DB 1; Length 220;
Best Local Similarity 25.4%; Pred. No. 0.0081;
Matches 53; Conservative 44; Mismatches 93; Indels 19; Gaps 10;
CC
QY 32 LVQTH--LKVQVTLCCALVASAGAYLILNLI--GGILTTMACGSMWLLSAPPYQ- 86
DB 14 LMTNKHVLRNTYELGLGLTAFSAVAIYISLNLPRPGILMLAGFYGLLFL----TVKL 69
QY 87 EQKRVALLMAAL--PEGASIGELIIBELGINDFP--SIVFGAFVG--CAVVGFCFSAAMALAR 142
DB 70 SNGSIGLILSFAFTGFLVGLTGLPILNVVSHGAGDIVLALAGTAATVAFAC--GAYVLT 127
QY 143 RREYLYLGLLSGVLLFWLHFASSIFGSMVAFKELYFGLLVFGYIVFDICIEIEK 202
DB 128 KQMSFLSGTIFALFVILLGWSVFFSPMLYTAISGLFVVFSTLGL--IYETSNII-- 194
QY 203 AHLGDMDYVKHALTFTDFGAFVRLII 231
DB 185 -HGNETYIRATWSIFVSLYNLFISLNI 212
CC
RESULT 13
Y893 DEIRA STANDARD; PRT; 231 AA.
AC Q9RVX6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein DR0893.
GN DR0893.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
CX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC -!- SIMILARITY: BELONGS TO THE BII FAMILY.
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CC -----
CC EMBL; AB001942; AAF10471.1; -
CC TIGR; DR0893; -
CC InterPro; IPR002199; Bax_inhbt1.
CC Pfam; PF01027; UPF0005; 1.
CC Hypothetical protein; Transmembrane; Complete proteome.
CC TRANSMEM 26 46 POTENTIAL.
CC TRANSMEM 56 76 POTENTIAL.
CC TRANSMEM 84 104 POTENTIAL.
CC TRANSMEM 112 132 POTENTIAL.
CC TRANSMEM 142 162 POTENTIAL.
CC TRANSMEM 163 183 POTENTIAL.
CC TRANSMEM 206 226 POTENTIAL.
CC SEQUENCE 231 AA; 24447 MW; BBB7D76A6445D9C9 CRC64;
CC -----
Query Match 9.7%; Score 124; DB 1; Length 231;
Best Local Similarity 26.2%; Pred. No. 0.011;
Matches 62; Conservative 41; Mismatches 94; Indels 40; Gaps 10;
CC
QY 23 LKNPQIGPLVQVTHLKQV-----YLTLCALVASAGAYL-----HILWNIQGL-LTT 69
DB 2 VLSMQLIANTQKTLQDQVTFWARTYSMAAGLALTAGVAVLTAQNEGLAMQVASLRPL 61
QY 70 MACGSMWLLSAPPYQKRVALLMAALPEG-ASIGPLI--ELGINFDPISVFGAFVG 126
DB 62 MLAQALVFLVS---MFAQRLSAAVAGALFVGVAULTGLTFSALLFAYSAPAAVITAFV 117
QY 127 CAVVGFCFSAAMALAR-----REYLYLGLLSGVLLFWLHFASSIFGSMVAFKFE 180
DB 118 SAGTGLMSVAGFVKIKDLSAMGRFFLF--AVLGLVAMLV-----NLFVGSALSIGI 169
QY 181 LYFGLLVFGYIVFDIQBIIEKAHLG-----DMDYVKHALTFTDFGAFVRLII 231
DB 170 SMIGVFLFAGLTAYDTQMLRNALSGISGEQASINGALALYLDIFNIFLFLNI 226
CC
RESULT 14
Y236 CAMJE STANDARD; PRT; 231 AA.
AC Q9PIQ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Cj0236c.
GN Cj0236c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
CX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150312; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holt R.D.,
RA Jorgensen F., Karpman A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BII FAMILY.
CC -----
```



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DR EMBL; AL139074; CAB72705.1; -  
DR InterPro; IPR002199; Bax\_inhbr1.  
DR Pfam; PF01027; UPF0005; I.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 36 56 POTENTIAL.  
FT TRANSMEM 58 78 POTENTIAL.  
FT TRANSMEM 83 103 POTENTIAL.  
FT TRANSMEM 143 163 POTENTIAL.  
FT TRANSMEM 170 190 POTENTIAL.  
SQ SEQUENCE 231 AA; 25487 MW; 279E67CA380336C9 CRC64;

Query Match 9.7%; Score 123.5; DB 1; Length 231;  
Best Local Similarity 26.8%; Pred. No. 0.012;  
Matches 62; Conservative 38; Mismatches 100; Indels 31; Gaps 10;  
QY 20 YDSLKNFRQI-SPLVOTLTKQVYLTCALVASAAGAYLHL-----WNIGLLTVAACMG 74  
DB 8 YSRSEFENTRSELSIRIKQYQLFAASLLAATVGAVGIFALASPIQSQVTFWLFA 67  
QY 75 SMVLLSAPPYQEQKRVALLMAALF-----EGASIGPLI--ELGINFDPISIVFGAFVC 127  
DB 68 VRIGLLFA--LQMKREAPLNVLVFGTFSGTLTLPILISVLALPAGGIIIAQAFALT 125  
QY 128 AVVFGCFGAAMLRREVLVGG-----LSSGVSLFLWLFHFASSIFGSGMAVFKPELY 182  
DB 126 TVAFAGLSVFAM-NTKKFTVNGKALFVLIVVAASLLNLFSSIVNLAISA----- 178  
QY 183 FGLLVFGVIVDTQEIIEKAHLGDMY-VKHALTLFTDFGAVFVRLIIM 232  
DB 179 VAAILFSFYLYDTQNIIR---GNVETPIEGAVLYLDFVNLVLSLNL 225

## RESULT 15

ID YBHL\_ECOLI STANDARD; PR7; 234 AA.  
AC P75768;  
DT 15-JUL-1998 (Ref. 36, Created)  
DT 15-JUL-1998 (Ref. 36, Last sequence update)  
DT 16-OCT-2001 (Ref. 40, Last annotation update)  
DE Hypothetical protein ybhl.  
GN YBHL OR B0786.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.,  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res 3:137-155 (1996).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.

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DR EMBL; AE000181; AAC73873.1; -  
DR EMBL; D90716; BAA35444.1; -  
DR EcoGene; EG13668; ybhl.  
DR InterPro; IPR002199; Bax\_inhbr1.  
DR Pfam; PF01027; UPF0005; I.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 24 44 POTENTIAL.  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 80 100 POTENTIAL.  
FT TRANSMEM 103 123 POTENTIAL.  
FT TRANSMEM 137 157 POTENTIAL.  
FT TRANSMEM 164 184 POTENTIAL.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 234 AA; 25902 MW; 7A59105563D5DFC8 CRC64;

Query Match 9.6%; Score 122; DB 1; Length 234;  
Best Local Similarity 25.5%; Pred. No. 0.016;  
Matches 59; Conservative 41; Mismatches 81; Indels 50; Gaps 11;  
QY 33 VQTHLKQVY-----ITLCCALVASAAGAYLHLWN-----IGLLTMA---CMGSM 76  
DB 17 LQYMAQYGYWMTVGLLITAFVAVYAANSAVMELLFTNRVFLIGLIIAQLALVIVLSAM 76  
QY 77 VMLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINPDPSIVFGAFVCAVFGCPFA 136  
DB 77 IQKLSA-----GVTTMLFMYLSALTGLTSSIF---IVYTAASIASTFFVTAGMFGMSL 128  
QY 137 AAMLARR-----REYLY---LGLLSGVSLFLFWLHFASSIFGSGMAVFKFELYFGLLYF 188  
DB 129 YGYTTKRDLSGFGNMLFWALIGIVLASLVN--FWLK-----SEALMWAVTYIGVIVF 178  
QY 189 VGYIVDFDQEI---EKHLGDMYVXH-----ALTLFTDFGAVFVRLIIL 231  
DB 179 VGLTAYDTQKLNWGEQIDTRDTSNLRKYSILGALTLYLDFINLFLMLLRI 229

Search completed: May 25, 2003, 12:21:40  
Job time : 39 secs



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OM protein - protein search, using sw model

Run on: May 25, 2003, 12:05:29 ; Search time 58 Seconds  
(without alignments)  
881.029 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272  
Sequence: 1 MEGTSPFDSQASRNWSY.....LIIMLNASEKEKKKRN 248

Scoring table: BLOSUM62

Gapoq 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:  
1: sp archaea.\*  
2: sp bacteria.\*  
3: sp fungi.\*  
4: sp human.\*  
5: sp invertebrate.\*  
6: sp mammal.\*  
7: sp mhc.\*  
8: sp organelle.\*  
9: sp phage.\*  
10: sp plant.\*  
11: sp rodent.\*  
12: sp virus.\*  
13: sp vertebrate.\*  
14: sp unclassified.\*  
15: sp virus.\*  
16: sp bacteriap.\*  
17: sp archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1134.5	89.2	249	10 Q93XB9	Q93XB9 nicotiana t
2	1010.5	79.4	247	10 Q93XC0	Q93XC0 brassica ra
3	1002.5	78.8	246	10 Q8W196	Q8W196 brassica ol
4	883	69.4	247	10 Q93XL2	Q93XL2 hordeum vul
5	490.5	38.6	237	11 Q9D2C7	Q9D2C7 mus musculu
6	472	37.1	262	10 Q23599	Q23599 arabidopsis
7	435.5	34.2	187	10 Q9L7B6	Q9L7B6 arabidopsis
8	192	15.1	305	5 Q9VIB2	Q9VIB2 drosophila
9	192	15.1	365	5 Q8T824	Q8T824 drosophila
10	174.5	13.7	219	16 Q8ZQ61	Q8ZQ61 salmonella
11	172	13.5	341	5 Q9VZ34	Q9VZ34 drosophila
12	171	13.4	346	11 Q91VC9	Q91VC9 mus musculu
13	170.5	13.4	219	16 Q8Z7R5	Q8Z7R5 salmonella
14	164	12.9	99	6 Q95309	Q95309 sus.scrofa
15	157.5	12.4	219	16 Q8XD81	Q8XD81 escherichia
16	150	11.8	233	16 Q8Y034	Q8Y034 ralstonia s

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17 144 11.3 266 3 074888 074888 schizosacch
18 143.5 11.3 342 5 P91373 P91373 caenorthabdi
19 141.5 11.1 237 12 Q8V310 Q8V310 camelbox vi
20 141.5 11.1 237 12 Q8Q086 Q8Q086 camelbox vi
21 136.5 10.7 245 16 Q8YEL9 Q8YEL9 bruceella me
22 132 10.4 319 4 Q9Y6G2 Q9Y6G2 homo sapien
23 131.5 10.3 228 12 Q8QRT8 Q8QRT8 chimpanzee
24 128 10.1 236 16 Q8ZGM1 Q8ZGM1 yersinia pe
25 124.5 9.8 239 10 Q9M1V9 Q9M1V9 arabidopsis
26 123 9.7 316 5 Q95T37 Q95T37 drosophila
27 123 9.7 324 5 Q9V6H7 Q9V6H7 drosophila
28 122 9.6 234 16 Q8X804 Q8X804 escherichia
29 119 9.4 284 4 Q9HCL9 Q9HCL9 homo sapien
30 118.5 9.3 239 5 Q9V6H6 Q9V6H6 drosophila
31 117.5 9.2 245 16 Q92L61 Q92L61 rhizobium m
32 116 9.1 244 5 Q8T8W2 Q8T8W2 drosophila
33 113.5 8.9 229 10 Q94GN3 Q94GN3 oryza sativ
34 113 8.9 210 12 Q72763 Q72763 cowpox viru
35 112 8.8 232 16 Q822Q4 Q822Q4 salmonella
36 112 8.8 256 10 Q94A20 Q94A20 arabidopsis
37 111 8.7 232 16 Q8ZKW9 Q8ZKW9 agrobacteri
38 109 8.6 260 16 Q8UC16 Q8UC16 agrobacteri
39 109 8.6 311 4 Q869X1 Q869X1 homo sapien
40 109 8.6 311 4 Q8TAM3 Q8TAM3 homo sapien
41 108.5 8.5 1107 10 Q9ATP8 Q9ATP8 acetabulari
42 108.5 8.5 1112 10 Q9FNX2 Q9FNX2 acetabulari
43 106 8.3 234 16 Q8ZQP9 Q8ZQP9 salmonella
44 106 8.3 284 5 Q9VFM3 Q9VFM3 drosophila
45 106 8.3 659 16 Q8Y6E1 Q8Y6E1 listeria mo

```

## ALIGNMENTS

### RESULT 1

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Q93XB9 ID Q93XB9 PRELIMINARY; PRT; 249 AA.
AC Q93XB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN Bi-1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SR-1; TISSUE=LEAF;
RA Boiduc N., Pitre F., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Nicotiana tabacum.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390556; AAK73102.1; -.
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UFF0005; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 249 AA; 27604 MW; 776EC35BEFB9F8 CRC64;

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Query Match 89.2%; Score 1134.5; DB 10; Length 249;

Best Local Similarity 87.1%; Pred. No. 5.7e-92;

Matches 217; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSA-SRNWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHI 59

Db 1 MESCSTFFNSQSSASRNWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHI 60

QY 60 LNNIGLLTTWACGSMYVLLSAPPYQEQEVALMAALPEGASIGLIELGINTDPSI 119

Db 61 LNNIGLLTTGCGVSGVILWMLMATPLYBEQKRIALLMAALFKGASIGLIELAIDFDSI 120

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QY 120 VFAGVGCVAVFCFSAAMARRRRLYLGLLSSGVLLFWLHFASSIFGGSMAVFKF 179
Db 121 VIGAFVGCVAVFCFSAAMARRRRLYLGLLSSGVLLFWLHFASSIFGGSMAVFKF 180
QY 180 ELYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASEK 239
Db 181 EVYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASK 240
QY 240 EEKKKRRN 248
Db 241 EEKKKRRN 249

RESULT 2
Q93XC0 PRELIMINARY; PRT; 247 AA.
AC Q93XC0;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1 (Bax inhibitor-like protein).
GN B1-1 OR B11.
OS Brassica napus (Rape), and
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708, 3712;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-B.napus; STRAIN=CV. WESTAR; TISSUE=LEAF;
RA Belduc N., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Brassica napus.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-B.oleracea;
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and B1: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF3101.1; -.
DR EMBL; AF453320; AAL50979.1; -.
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 247 AA; 27526 MW; F5A5B5E6FD4E8DB_CRC64;

Query Match 79.4%; Score 1010.5; DB 10; Length 247;
Best Local Similarity 75.4%; Pred. No. 4.5e-81;
Matches 187; Conservative 35; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSASRNWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHL 60
Db 1 MDSFSPFDSQSGRS-WSYDSLKNLRQISPSVQNLKRVYLTLCALVASAFAYLHL 59
QY 61 WNIGGLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGLIELGNFDPSTV 120
Db 60 WNIGGLTTTACGTMWLLSCPPYEQKRLSLFLSAVLEGASVGLIKVAVDFPSIL 119
QY 121 FGAFVGCVAVFCFSAAMARRRRLYLGLLSSGVLLFWLHFASSIFGGSMAVFKFE 180
Db 120 ITAFVGTAFICFSGAAMLARREYLILGLLSSGLSMLMWLQFASIFGGSASIFKFE 179
QY 181 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASEKE 240
Db 180 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASK 239
QY 241 EEKKKRRN 248
Db 240 EEKKKRRN 245

RESULT 4
Q93XL2 PRELIMINARY; PRT; 247 AA.
AC Q93XL2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN B1-1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

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Db 240 DKKKRRN 247

RESULT 3
Q8W196 PRELIMINARY; PRT; 246 AA.
AC Q8W196;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Bax inhibitor-like protein.
GN B12.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and B1: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453321; AAL50980.1; -.
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E_CRC64;

Query Match 78.8%; Score 1002.5; DB 10; Length 246;
Best Local Similarity 76.0%; Pred. No. 2.2e-80;
Matches 187; Conservative 33; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSASRNWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHL 60
Db 1 MDSFSPFDSQSGRS-WSYDSLKNLRQISPSVQNLKRVYLTLCALVASAFAYLHL 59
QY 61 WNIGGLTTMACGSMWLLSAPPYQEQKRVALLMAALFEGASIGLIELGNFDPSTV 120
Db 60 WNIGGLTTTACGTMWLLSCPPYEQKRLSLFLSAVLEGASVGLIKVAVDFPSIL 119
QY 121 FGAFVGCVAVFCFSAAMARRRRLYLGLLSSGVLLFWLHFASSIFGGSMAVFKFE 180
Db 120 ITAFVGTAFICFSGAAMLARREYLILGLLSSGLSMLMWLQFASIFGGSASIFKFE 179
QY 181 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASEKE 240
Db 180 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLNASK 239
QY 241 EEKKKRRN 246
Db 240 EEKKKRRN 245

RESULT 4
Q93XL2 PRELIMINARY; PRT; 247 AA.
AC Q93XL2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN B1-1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

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DB 145 GFGAKQLAWLHVCAVL-GAVLAPMCLLG-----GPILTKALLYTSGIVGALSTVAACAPSE 199
QY 145 EYLVLGGLSSGVSLF-----WLHFASIFGSGMAVFKFELYFGLLVFVGYIVFDIQ 197
DB 200 KFLHMGGLPLAIGLVFVPASSLASWMLPPTTAVGAG---LASMSLYGGLILFSGFLLYDTQ 256
QY 198 EIEKAHLGDM-----DYVKAHLTFTDFGAVFVRILIMLNKASEKEKKKRN 248
DB 257 RIVKSAELYPOYSKFPYDPINHALAIYDNLNIFIRIAILAGD-----QKRN 305

RESULT 9
Q87824 PRELIMINARY; PRT; 365 AA.
AC Q87824
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE AT14090p.
GN CG1287.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075204; AAL68072.1; -.
SQ SEQUENCE 365 AA; 39108 MW; 676C61176F923745 CRC64;

Query Match 15.1%; Score 192; DB 5; Length 365;
Best Local Similarity 25.1%; Pred. No. 5.6e-09;
Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;

QY 36 HLKQVYLTLCALVASAGY-----LHILNIGLLTTWACM-----GSMVWLSAPP 84
DB 145 HATYAFGASCGVTAAVAFFQSDAMMALTRSGWASVLTGLVMSLSIAQGLGYQP 204
QY 85 YOEQRVALLMAALFEGASIGLIELGINFDPISIVFGAVGCVGFCFSAAMLARR 144
DB 205 GFGAKQLAWLHVCAVL-GAVLAPMCLLG---GPILTKALLYTSGIVGALSTVAACAPSE 259
QY 145 EYLVLGGLSSGVSLF-----WLHFASIFGSGMAVFKFELYFGLLVFVGYIVFDIQ 197
DB 260 KFLHMGGLPLAIGLVFVPASSLASWMLPPTTAVGAG---LASMSLYGGLILFSGFLLYDTQ 316
QY 198 EIEKAHLGDM-----DYVKAHLTFTDFGAVFVRILIMLNKASEKEKKKRN 248
DB 317 RIVKSAELYPOYSKFPYDPINHALAIYDNLNIFIRIAILAGD-----QKRN 365

RESULT 10
Q82061 PRELIMINARY; PRT; 219 AA.
AC Q82061
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Putative TEGT family carrier/transport protein.
GN YCCA OR STM1085.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella
OX NCBI_TaxID=602;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2."
RL Nature 413:852-856 (2001).
DR EMBL; AE008747; AAL20018.1; -.
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN_1.
KW Hypothetical protein, Complete proteome.
SQ SEQUENCE 219 AA; 23313 MW; 9FA28BACE70B8497 CRC64;

Query Match 13.7%; Score 174.5; DB 16; Length 219;
Best Local Similarity 29.6%; Pred. No. 1.1e-07;
Matches 67; Conservative 42; Mismatches 76; Indels 41; Gaps 11;

QY 27 RQISPLVQTH--LKQVY--LTICCALVASAGYHLHILNIGLLTTWACMGMVWLSA 82
DB 9 RDRSLLSTHKVLRNTYFLLSLTLASITATASTVIMLPSPGLILTVGMGLMFL---- 65
QY 83 PPYQ-EQKRVALLMAAL--FEGASIGLIELGINFDPISIVFG-AFVGCAVFGFCFAA 138
DB 66 -TYTANKPVGILLSAFATGTLGVLGILPINAVLSAGMGDVLGALGGTALVFFCCS-AY 123
QY 139 MLARREYVLGGLSSGVSLF-----WLHFASIFGSGMAVFKFELYFGLL 186
DB 124 VLTRKQMSFLGGMLMAGIVVVLIGWVNIQFLQPLALHLAIS-----AVF-----IL 170
QY 187 VFVGVIVFDTOEIIIEKAHLGDMYVKHALTFTDFGAVFVRILIM 232
DB 171 ISSGALLYETSNI--HGGETNVIKATVSLVSLYVSLIL 213

RESULT 11
Q9VZ34 PRELIMINARY; PRT; 341 AA.
AC Q9VZ34
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG2076 protein.
GN CG2076.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abille J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busem D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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RESULT 12	
Q91VC9	PRELIMINARY; PRT; 346 AA.
ID Q91VC9;	
AC Q91VC9;	
DT 01-DEC-2001 (TReMBUrel. 19, Created)	
DT 01-DEC-2001 (TReMBUrel. 19, Last sequence update)	
DT 01-JUN-2002 (TReMBUrel. 21, Last annotation update)	
DE Growth hormone-inducible membrane protein (Similar to FTD10 protein)	
DE (Hypothetical 37.3 kDa protein).	
GN GH1W.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
[1] RN	
SEQUENCE FROM N.A.	
RP STRAIN=C57BL/6;	
RC MEDLINE=21308975; PubMed=1416014;	
RX Li Y., Kelder B., Koepchick J.J.;	
RA "identification, isolation, and cloning of growth hormone (GH)-	
RT inducible interscapular brown adipose complementary deoxyribonucleic	
RT acid from GH antagonist mice." ;	
RL Endocrinology 142:2937-2945(2001) .	
RN [2]	

RESULT	ID	Q82R75	PRELIMINARY;	PRT;	219 AA.
DR	Q82R75				
AC	Q82R75;				
DT	01-NAR-2002 (TReMBLrel. 20, Created)				
DT	01-NAR-2002 (TReMBLrel. 20, Last sequence update)				
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)				
DE	Putative membrane protein.				
GN	STY1112				
OS	Salmonella typhi.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Salmonella.				
OX	NCBI_TaxID=601;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CT18;				
RC	MEDLINE=1534947; PubMed=11677608;				
RA	Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.				
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,				
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,				
RA	Cronin A., Davis P., Davies K.M., Dowd L., White N., Farrar J.,				
RA	Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,				
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,				
RA	Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,				
RA	Whitehead S., Barrall B.G.;				
RT	"Complete genome sequence of a multiple drug resistant Salmonella				
RT	enterica serovar Typhi CT18.";				
RL	Nature 413:848-852(2001).				
DR	EMBL; AL627269; CAD08212.1; --				
DR	InterPro; IPR002159; Bax_inh1b1.				
DR	Pfam; PF01027; UBF0005; 1.				
DR	PROSITE; PS01243; B11; UNKNOWN 1.				
KW	Hypothetical protein; Complete proteome.				
SC	SEQUENCE 219 AA: 23347 MW: 914561A8095F6E97 CRC64;				

Query Match 13.4%; Score 170.5; DB 16; Length 219;

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Best Local Similarity 29.2%; Pred. No. 2.5e-07;
Matches 66; Conservative 42; Mismatches 77; Indels 41; Gaps 11;

QY 27 ROISPLVQTH--LKQVY--LTCCALVASAAGAYLHILWNGIGLLTTMACGSMVWLLSA 82
Db 9 RDRSSLLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGILILVGMVGLMFL--- 65
QY 83 PPYQ-EQKREVALMAAL--FEGASIGPLIELGINFDPISIVFG-AFVGCNAVFCFSA 138
Db 66 -TVKTANKPVGILSAFAFTGFLGYILGPILNAYLSAGMGDVIGALGALTALVFFCCS-AY 123
QY 139 MLARREYVLGLGLSSGVSLAF-----WLHPASSIFGSMAYVFKELYFGLL 186
Db 124 VLTRKDMGFLGMLMAGIVVVLIGWNIPLQALHLAIS-----AVF-----IL 170
QY 187 VFGYIVFTDTEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIM 232
Db 171 ISSGALYETSNII---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

RESULT 14
Q95309 PRELIMINARY; PRT; 99 AA.
AC Q95309;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TEGT protein (fragment).
GN TEGT.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81159; CAB03546.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
FT NON TER 99
SQ SEQUENCE 99 AA; 10846 MW; EA009C94B5BE6211 CRC64;

Query Match 12.9%; Score 164; DB 6; Length 99;
Best Local Similarity 36.3%; Pred. No. 4e-07;
Matches 33; Conservative 19; Mismatches 35; Indels 4; Gaps 2;

QY 19 SYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHILWNI--GGLITTMACGSM 76
Db 9 NFDALLKFSHTPTQHLKKVYASFALCNFVAAGAYVHVVTFTQAGLLSGLGLIM 68
QY 77 VWLSAPPYQ--EQKREVALMAALFEGASI 105
Db 69 IWLWATPHSHETQKRLGLLAGFAFLTGVL 99

RESULT 15
Q8XD81 PRELIMINARY; PRT; 219 AA.
AC Q8XD81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative carrier/transport protein.
GN YCCA OR Z1322 OR ECS1054.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
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SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).

SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 050952;
RX MEDLINE=2115823; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AB005287; AAG55456.1; -
DR EMBL; AP002554; BAB34477.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 23393 MW; 1AD9F28528D32FFE CRC64;

Query Match 12.4%; Score 157.5; DB 16; Length 219;
Best Local Similarity 26.7%; Pred. No. 3.5e-06;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASRNRWSYDLSLKNFRQISPLVQTH--LKQVY--LTCCALVASAAGAYLHILWNGIGLL 67
Db 6 SSSHRTS-----LLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPFGLI 53
QY 68 TTMACGSMVWLLSAAPPYQEQKREVALMAAL--FEGASIGPLIELGINFD-PSIVFGAF 124
Db 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGTLGFLGYILGPILNAYLSAGMGDVIAAL 110
QY 125 VGCNAVFCFSAAMLARREYVLGLGLSSGVSLF-----WLHPASSIFGG 172
Db 111 GGTALVFFCCS-AYVLTTRKDMGFLGMLMAGIVVVLIGWNIPLQALHLAIS----- 165
QY 173 SXAVFKELYFGLLVFGYIVFTDTEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIM 232
Db 166 --AVF-----ILISSGAILPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

Search completed: May 25, 2003, 12:22:52
Job time : 61 secs
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